

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:15:24 ; Search time 121.13 Seconds
(without alignments)
283.778 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPTTYLLLLLLL.....RPGQVPPVSPQDLILLVH 235

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*

1: sp-archaea.*

2: sp-bacteria.*

3: sp-fungi.*

4: sp-human.*

5: sp-invertebrate.*

6: sp-mammal.*

7: sp-mhc.*

8: sp-organelle.*

9: sp-phage.*

10: sp-plant.*

11: sp-rodent.*

12: sp-virus.*

13: sp-invertebrate.*

14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	Q9MZV0	Q9MZV0 canis famil
2	894.5	72.0	291	Q9MZU9	Q9MZU9 felis silve
3	840	67.6	292	Q9GKE0	Q9GKE0 bos taurus
4	746	60.1	274	Q9GKD9	Q9GKD9 bos taurus
5	602.5	48.5	172	Q81104	Q81104 mus musculu
6	112.5	9.1	579	Q9LGG8	Q9LGG8 oryza sativ
7	95.5	7.7	1240	Q9DWH8	Q9DWH8 rat cytomeg
8	93.5	7.5	658	Q9C570	Q9C570 arabidopsis
9	93	7.5	1217	Q17889	Q17889 caenorhabdi
10	92	7.4	251	Q9HAD2	Q9HAD2 homo sapien
11	90.5	7.3	5120	Q9PU36	Q9PU36 gallus gall
12	89.5	7.2	474	Q17610	Q17610 caenorhabdi
13	88.5	7.1	270	Q9UMT1	Q9UMT1 homo sapien
14	88.5	7.1	404	Q9AWJ4	Q9AWJ4 oryza sativ
15	88.5	7.1	1386	Q75064	Q75064 homo sapien
16	88	7.1	250	Q9GKE2	Q9GKE2 mus musculu
17	88	7.1	675	Q9DBT2	Q9DBT2 mus musculu
18	88	7.1	753	Q56971	Q56971 kenedya ye
19	87.5	7.0	470	Q9L0I1	Q9L0I1 arabidopsis

20	87.5	7.0	946	10	Q22015	O22015 cylindrothe
21	87	7.0	510	5	Q44018	Q44018 leishmania
22	86.5	7.0	299	6	Q9TTT9	Q9TTT9 bos taurus
23	86	6.9	255	11	Q9D3J3	Q9D3J3 mus musculu
24	86	6.9	299	12	Q84647	Q84647 paramesium
25	86	6.9	746	5	Q23600	Q23600 caenorhabdi
26	86	6.9	911	11	Q35407	Q35407 mus musculu
27	85	6.8	282	4	Q9BSA1	Q9BSA1 homo sapien
28	85	6.8	289	2	Q9A3K1	Q9A3K1 caulobacter
29	85	6.8	413	11	Q99MM1	Q99MM1 mus musculu
30	85	6.8	1217	4	Q9P2D0	Q9P2D0 homo sapien
31	84.5	6.8	932	11	Q99JH4	Q99JH4 mus musculu
32	84.5	6.8	3726	11	Q61329	Q61329 mus musculu
33	84	6.8	220	4	Q96030	Q96030 homo sapien
34	84	6.8	224	6	Q19031	Q19031 ovis aries
35	84	6.8	263	12	Q36417	Q36417 alcelaphine
36	84	6.8	567	11	Q99J43	Q99J43 mus musculu
37	84	6.8	687	4	Q9H975	Q9H975 homo sapien
38	84	6.8	1234	11	Q9R044	Q9R044 rattus norv
39	84	6.8	1252	11	Q9QXX7	Q9QXX7 rattus norv
40	84	6.8	1252	11	Q9JIX2	Q9JIX2 rattus norv
41	83.5	6.7	199	2	Q9RZL3	Q9RZL3 deinococcus
42	83.5	6.7	290	10	Q9FUH0	Q9FUH0 medicago tr
43	83.5	6.7	524	5	Q9NK88	Q9NK88 drosophila
44	83.5	6.7	530	12	Q07701	Q07701 herpesvirus
45	83.5	6.7	548	5	Q9VJP2	Q9VJP2 drosophila

ALIGNMENTS

RESULT 1

Q9MZV0
ID Q9MZV0 PRELIMINARY; PRT; 294 AA.
AC Q9MZV0;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMREL. 15, Last annotation update)
DE FLT3 LIGAND.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RL long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155148; AAF87088.1;
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match 72.1%; Score 895.5; DB 6; Length 294;
Best Local Similarity 77.1%; Pred. No. 6.6e-77;
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;
QY 1 MVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
DB 1 MVLAPAWSPTASLLLLLLSPGLRGTPDCSFHSPISSDFAVKIRELSYLLQDPVTV 60
QY 61 ASNLQDELGGWRLVLAQRWMLKTVAGSKMGLLVRNTEIHFVTKCAFOPPPSCL 120
DB 61 ASNLQDELGGWRLVLAQRWMLKTVAGSKMGLLVRNTEIHFVTKCAFOPPPSCL 120
QY 121 RFVQTNISRLQETSEOLVAKPWITRONFSRCLELQCPDSSSTLPPSPRLEATPT 180
DB 121 RFVQTNISRLQETSEOLVAKPWITRONFSRCLELQCPDSSSTLPPSPRLEATPT 180
QY 181 APQPP-LLLLLLPVGILLAAWCLHW-QTRRTTPRPGEQVPPVS-----PQD 229
DB 181 APQPP-LLLLLLPVGILLAAWCLHW-QTRRTTPRPGEQVPPVS-----PQD 229

Db 181 AFQAPRLLLLLLPPVALLMSTAMWCLHWRRRRRRRRSPYFGEQRTLRPSRSHLPED 236

RESULT 2

Q9MZU9 ID Q9MZU9 PRELIMINARY; PRT; 291 AA.
AC Q9MZU9; DB 6; Length 291;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE FLT3 LIGAND.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155149; AAF87089.1; -- 32459 MW; 8F85A10A5EA0DCC6 CRC64;
SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;
Best Local Similarity 80.5%; Pred. No. 8.1e-77;
Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MVLAPAWSPPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
Db 1 MVLAPAWSPPTT-SLLLLLLSPGLQGTDCSFHSPISSTFVKIRKLSYLLQDYPVT 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATPT 180
QY 181 AFQAPP-LLLLLLPVGLLLAAWCLHWQRTTTPRPEQ 220
Db 181 AFQAPP-LLLLLLPVGLLLAAWCLHWQRTTTPRPEQ 221

RESULT 3

Q9GKEO ID Q9GKEO PRELIMINARY; PRT; 292 AA.
AC Q9GKEO; DB 6; Length 292;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE FLT3 LIGAND ISOFORM-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11120823;
RA Wangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF9322.1; -- 32390 MW; D68B9ED79221202D CRC64;
SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;
Best Local Similarity 76.3%; Pred. No. 1.2e-71;
Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;
QY 1 MVLAPAWSPPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MVLAPAWSPPTT-SLLLLLLSPGLQGTDCSFHSPISSTFVKIRKLSYLLQDYPVT 60
QY 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 119
Db 61 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 120
QY 120 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATAP 179
Db 121 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATAP 180
QY 180 TAPQPP-LLLLLLPVGLLLAAWCLHWQRTTTPRPEQ 220
Db 181 PGQSPPLLLLLLPVALLMSTAMWCLHWRRRRRRTRYPGER 224

RESULT 4

Q9GKD9 ID Q9GKD9 PRELIMINARY; PRT; 274 AA.
AC Q9GKD9; DB 6; Length 274;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE FLT3 LIGAND ISOFORM-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11120823;
RA Wangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282986; AAF9323.1; -- 30372 MW; 725A7F77A95DA98B CRC64;
SQ SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match 60.1%; Score 746; DB 6; Length 274;
Best Local Similarity 69.6%; Pred. No. 8.6e-63;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

QY 1 MVLAPAWSPPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MVLAPAWSPPTT-SLLLLLLSPGLQGTDCSFHSPISSTFVKIRKLSYLLQDYPVT 60
QY 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 119
Db 61 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 114
QY 120 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATAP 179
Db 115 -----QDTHQQLQALKPWITRONFSRCLELQCCQDPSSTLPPSPRPLEATAP 162
QY 180 TAPQPP-LLLLLLPVGLLLAAWCLHWQRTTTPRPEQ 220
Db 163 PGQSPPLLLLLLPVALLMSTAMWCLHWRRRRRRTRYPGER 206

RESULT 5

Q61104 ID Q61104 PRELIMINARY; PRT; 172 AA.
AC Q61104;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

```

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE FLT3 LIGAND, T169 FORM.
GN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.G., Rosnet O.,
RA Birnbaum D., Hannum C.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44024; AA93305.1;
DR MGD; MGI:95560; FLT3L.
SQ SEQUENCE 172 AA; 19465 MW; 04F0A010171E3384 CRC64;

Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 2e-49;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;

Qy 1 MTVLAPANSP-TTYILLLLSSGSLGTCDFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MTVLAPANSPNSLLLLLSPLCLRGTPDCYFESHSPISSENFVKFRELTHLLKDYPT 60
Qy 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLRLVTEIHFVTKCAFQPPPS 119
Db 61 VAVNLQDEKHKALNSLFLAQRWILQKTVAGSKMOTLLEDVTEIHFVTSCTFQPLPEC 120
Qy 120 LRFVQTNSRLQETSEQLVAKPWITR--QNFSCLELQCPDSDSTL 165
Db 121 LRFVQTNSHLLKDCPTQLLALKPCIGKACQNFSCLELQCPDSDSL 168

RESULT 6
Q9LGG8 PRELIMINARY; PRT; 579 AA.
ID Q9LGG8
AC Q9LGG8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE EXTENSIN-LIKE PROTEIN.
GN P0406H10.6 OR OJ1174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
clone:P0406H10."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, BAC
clone:OJ1174_D05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002524; BAB07956.1;
DR EMBL; AP003118; BAB33013.1;
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR002965; P_rich_extensn.
DR InterPro; IPR000504; RRM.
DR Pfam; PF00560; LRR; 2
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00370; LRR; 5.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

```

```

SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;
Best Local Similarity 23.7%; Pred. No. 0.018;
Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

Qy 17 LLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRL 76
Db 244 ILLINTGLS-----SCLPEVGM-LREVTVE-----DVSEFNLAGPLPSA 282
Qy 77 VLAQRWMLKTVAGSKMOGLLRLVTEIHFVTKCAFQ-----PPSCLRFV-----QT 125
Db 283 VAGNRKVEQL-DVAHNLITGAIPQVCELPRKKNFTFAYNFFFTGEPSCAHAVPRYGD RR 341
Qy 126 NI--SRLQETSEQLVAKPWITRQNF SR---CLELQCPDSDSTLPPKSPRPLEATAP 179
Db 342 NCLPNRPQORTLRQCAF-----FARPPVNCAAFQCKFFVPALPPSPPPP--SPPP 391
Qy 180 TAPQPPILLLLLPVGLLLAAWCLHWQTRRTTRPRGQVPPVPS 227
Db 392 PSPPPP-----SPPPSTSPPPSP 411

RESULT 7
Q9DWH8 PRELIMINARY; PRT; 1240 AA.
ID Q9DWH8
AC Q9DWH8
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE PR2.
GN R2.
OS Rat cytomegalovirus (strain Maastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome."
RL J. Virol. 74:7656-7665(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20473137; PubMed=11018281;
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
spliced transcript."
RL Virus Res. 69:119-130(2000).
DR EMBL; AF232689; AAF99111.1;
SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match 7.7%; Score 95.5; DB 12; Length 1240;
Best Local Similarity 33.0%; Pred. No. 1.7;
Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

Qy 160 PDSSTL-----PPWSPRP--LEAFTAPQP-PLLLLLLPVGLLLAA 201
Db 1060 PDSSTAVTGEATERTSPATPRYPLPGVDLSALPLAPQPTLLSLVPA----- 1112
Qy 202 AWCLHWQTRRTTRPRGQVPPVPSQD 229
Db 1113 -----QATRASPRPTDAPP-PTPAD 1132

RESULT 8
Q9C5T0 PRELIMINARY; PRT; 658 AA.
ID Q9C5T0
AC Q9C5T0;

```



```
Db 76 "PPGPPRLPCSGSTPGPRLLPQ-----ALAPPGHCGFSS--RFWFHRTTQAPPPG 127
QY 170 SRPL-EATAP-----TAPOPLLLLLPVGLLLAAWCLHWQTRRRTPRPG 218
Db 128 PRPLPQALVPDPHSGSPRTTQAPLL-----W-LHPRTT--QTPPPG 169
QY 219 EQVPPVPSQDLL-LVEH 235
Db 170 ---PPRPLPQALPQDH 184

RESULT 11
Q9PU36 PRELIMINARY; PRT; 5120 AA.
ID Q9PU36
AC Q9PU36;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE ACZONTN (FRAGMENT).
GN ACZ.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RL TISSUE-BRAIN;
RX MEDLINE=94439764; PubMed=10508862;
RA Wang X., Kirschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RA Klimann M.W.;
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin.";
RL J. Cell Biol. 147:151-162(1999).
DR EMBL; Y19187; CAB60725.1; -.
DR HSP; P04410; IJ25.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR Pfam; PF00595; PDZ; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRINTS; PR00399; SYNAPTOTAGM.
DR SMART; SM00239; C2; 2.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE; PS00004; C2_DOMAIN_2; 2.
DR PROSITE; PS0106; PDZ; 1.
FT NON_TER 1
SQ SEQUENCE 5120 AA; 560760 MW; A658D9891B65B412 CRC64;

Query Match 7.3%; Score 90.5; DB 13; Length 5120;
Best Local Similarity 24.3%; Pred. No. 22;
Matches 45; Conservative 19; Mismatches 72; Indels 49; Gaps 7;

QY 90 AGSKMOGLLRVNTETIHF-----VTKCAFOPPPSCSLRFVQTN----- 126
Db 224 AARKMSTVETGIKIHEDSHKSLDMTRINLTGTSETQOPPLCVASVYKEPASETPA 2283
QY 127 --ISRLQETSE-QLVAKPKWITQNF-----SRCLELQCPDSTLPPSPRPLEATAP 179
Db 2284 VPTPRVSVKTSVMSPPSAFALTSKVSFSLRSSLDSPAQFSPSPPPPPPPPPPLPPP 2343
QY 180 TAPQ-----PLLLLLPVGLLLAAWCLH-WQTRRTTPRGEQV 221
Db 2344 ILPKPAIYPKKSQIQAPMATATAPVPLVTSVATLESAAVLKNHVPVTKTYTTP-PPV 2402
QY 222 PPVPS 226
|||
```

```
Db 2403 PPKPS 2407

RESULT 12
O17610 PRELIMINARY; PRT; 474 AA.
ID O17610
AC O17610;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE C28D4.2 PROTEIN.
GN C28D4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z82259; CAB05129.1; -.
DR InterPro; IPR002573; Choline_kinase.
DR Pfam; PF01633; Choline_kinase; 1.
SQ SEQUENCE 474 AA; 54628 MW; DDF11C97A1542FFC CRC64;

Query Match 7.2%; Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%; Pred. No. 2.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDPYVTVASNLQDEELCGGLWRL 76
Db 65 TDCVDLKKVFSKFSAPISGEILFRFLCAKYL-----GGAWRK 106
QY 77 VLAQRWMERLKTVAGSKMOGLLRVNTETIHFVTKCAFOPPPSCSLR-FVQTNISRLQET- 134
Db 107 VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIOPEKALLRHVCSDIDLLSESV 162
QY 135 -----SEQLVAKPKWITQNFSCLELQ-----QPDSTLPPSPR--PLEATA 178
Db 163 VETLLSERNLGPKMLGVFGGRFEQIPSRALQCLSKLGLSLKLTAPIVAVRHTLDAP 222
QY 179 PTAPQPPPLLLLLPVGLLLAAWCLHWQTRRRTP-----RPGE-----QVPPVPSQD 229
Db 223 PKEPQ-----TLQTAQWLERF-----KKTAGERPIETMYLTQAKVKSDYPST 266
QY 230 LLVE 234
Db 267 ITVAQ 271

RESULT 13
Q9UMT1 PRELIMINARY; PRT; 270 AA.
ID Q9UMT1
AC Q9UMT1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE NKP44RG2 PROTEIN.
GN NKP44RG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID;
RA Cantoni C., Biasoni R.;
RT "NKP44 related genes.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ010100; CAB52290.1; -.
```

DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
SQ SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;
Best Local Similarity 23.0%; Pred. No. 1.5;
Matches 63; Conservative 22; Mismatches 112; Indels 77; Gaps 15;

QY 7 AWSPTTIVLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQD 66
Db 2 AWRALHPLLLLLLPFGSQAKQVLSVAGOTLTVRQ-----YPT----- 45
QY 67 EELCGGLW-----RLVLAQR-----WNERLKTAVGSKMQGLLRVNTETI- 105
Db 46 ----GSLYEKKGWCKEASALVCIRLVTSRPRTMANTSRF-TIWDPDAGFTVTMDLR 100
QY 106 -----HFVTKAFOPPPSCULRFVOTNISRLLOETSEOLVALKPWITRONFSRCLELQ-CQ 159
Db 101 EEDSGHY--WCRIYRPSD--NSVSKSVRFVLVSPASASTQTPTPRDLVSSQTQTQSCV 156
QY 160 PDS-----STLPPHSP-RPLEATAPQ-----PPLLLLLLPV--GLL--- 197
Db 157 PPTAGARQAPESPSTIVPSHPSPVPLFSPRPNSTLRPGPAAPALVPEVFCGLLVAK 216
QY 198 -LLAAACWCLHWQRTTRPRGEOV--PPVPSQ 228
Db 217 SLVLSALLVWVLRNHRHQGRSLHPAQRQ 250

RESULT 14

Q9AWJ4 PRELIMINARY; PRT; 404 AA.

AC Q9AWJ4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE P0489A05.3 PROTEIN.
GN P0489A05.3
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0489A05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003105; BAB32983.1;
SQ SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;
Best Local Similarity 26.1%; Pred. No. 2.3;
Matches 66; Conservative 24; Mismatches 88; Indels 75; Gaps 17;

QY 33 QHSPISDF--AVKIRELSYLLQDYPVTVASNL-----QDEELCGGLRLVL 78
Db 107 RHFSLFSFLEKVIQITPLKYVSNVNYPLKPNQTFITLNYQKNSEPOLCKRFW---- 162
QY 79 AQRWERLKTAVGSKMG-----LLRVNT--EIHFTKCAFOPPPSCLRFVOTNI---SRL 130
Db 163 -STWQSNAGAY-GSRAGGSERLRRSPWLPVPPPPPPRASLAAGVPNIATLSRA 220
QY 131 LOETSEOLVALKPWITRONFSR---CLELQ--CQDSSITL-----PPWSPRPLEAT 177
Db 221 LSATG-----TPTTSSSILRPLHCELLPLLRARPSLSPLPLLPQAPPHPLP---P 271

QY 178 APTAPQPPPLLLLLL-----PV---GLL-----LLAAACWCLHWQRTTRTPR 216
Db 272 PPTARAPPIAVLCRLCPLYLKPKPPVAGGLFVAHSALTAVLCAGCV--RLHRRPLR 329
QY 217 P-GEQVPPVPS 227
Db 330 PPSSELLPLSRAP 342
RESULT 15
O75064 PRELIMINARY; PRT; 1386 AA.
AC O75064;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE K1A00476 (TrEMBLrel. 17, Last annotation update)
DE KIAA0476 PROTEIN.
GN KIAA0476.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98116662; PubMed=9455484;
RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
RA Nomura N., Ohara O.;
RT "Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain."
RL DNA Res. 4:345-349(1997).
DR EMBL; AB007945; BAA32321.1;
DR InterPro: IPR001194; DENN.
DR InterPro: IPR002885; PPR.
DR Pfam: PF01535; PPR; 1.
DR Pfam: PF02141; DENN; 1.
SQ SEQUENCE 1386 AA; 152296 MW; BE960E7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;
Best Local Similarity 23.1%; Pred. No. 8.6;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;
QY 21 SSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELC---GGLWRL 76
Db 1104 SAGASGSKDAPVPGP-----GPVLSRRICLA--LDEPQLCNHMGASRR 1148
QY 77 VLAQRWERLKTAVGSKMGGLLRVNTETIHFVTKCAFOPPPSCLRFVOTNISRLLOETSE 136
Db 1149 VESGAWAYLSPLVLRKELESIVENEGSEV-----LALPELPSAHPFIWNLLWYFQL-- 1201
QY 137 QLVALKPWITRONFSRCLELOCO-PDSSTLPPPW-SPRPLEA-----TAPTAPQP 185
Db 1202 RLPSTLPGVLAS-----CDGPSHQAPSPMLTPDASVQVRLMDVLPDPNSCPP 1253
QY 186 LLLLLLPVGLLLAAACWCLHWQRTTRTPRGEQVPPVPSQDILLVE 234
Db 1254 LYVL-----WRVHSQ-IPQVWVPG-----PVPASLSLALLE 1284

Search completed: April 1, 2002, 06:25:43
Job time: 619 sec

Mon Apr 1 06:15:20 2002

us-08-162-407-6.rspt

Page 7

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 77.69 Seconds
(without alignments)
224.060 Million cell updates/sec

Title: US-08-162-407-6
Perfect score: 1242
Sequence: 1 MVLAPAWSPFTYLLLLLLL.....RPGQVPPVSPQDLLLVEH 235

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	16	AA67541
2	1242	100.0	235	20	AA67769
3	1242	100.0	235	21	AA69719
4	1242	100.0	235	22	AA620192
5	1236	99.5	235	16	AA66175
6	1236	99.5	235	22	AA620194
7	1124	90.5	212	21	AA69721
8	1114	89.7	209	19	AA69007
9	1114	89.7	209	21	AA69720
10	1110	89.4	209	21	AA69723
11	1110	89.4	209	21	AA69726

12	1110	89.4	209	21	AA69727	Human flt-3 mutein
13	1110	89.4	209	21	AA69729	Human flt-3 mutein
14	1108	89.2	209	21	AA69722	Human flt-3 mutein
15	1108	89.2	209	21	AA69724	Human flt-3 mutein
16	1107	89.1	209	21	AA69728	Human flt-3 mutein
17	1100	88.6	209	21	AA69725	Human flt-3 mutein
18	970	78.1	185	22	AA620195	Human flt-3 ligand
19	895.5	72.1	294	21	AA58204	Canine flt-3 ligand
20	894.5	72.0	291	21	AA58210	Feline flt-3 ligand
21	834	67.1	178	22	AA620193	Human flt-3 ligand
22	797.5	64.2	268	21	AA58206	Canine mature Flt-
23	796.5	64.1	276	21	AA58207	Canine flt-3 ligand
24	791.5	63.7	265	21	AA58211	Feline mature Flt-
25	768.5	61.9	231	16	AA67540	Mouse flt-3 ligand
26	768.5	61.9	231	20	AA67768	Murine flt-3 ligand
27	768.5	61.9	231	22	AA620186	Mouse flt-3 ligand
28	768	61.8	232	16	AA66177	Mouse flt-3 ligand
29	764	61.5	232	22	AA620189	Mouse flt-3 ligand
30	745	60.0	150	19	AA677930	Flt3 ligand FLT10C
31	745	60.0	150	19	AA669054	Human flt-3 receptor
32	740.5	59.6	377	19	AA678124	Chimeric receptor
33	739	59.5	143	19	AA677926	Flt3 ligand FLT3C
34	739	59.5	143	19	AA69050	Human flt-3 receptor
35	737.5	59.4	349	19	AA683289	Human flt-3 ligand
36	737.5	59.4	349	19	AA678005	Flt3L 1-139/IgG2b/
37	736.5	59.3	340	19	AA683291	Human flt-3 ligand
38	736.5	59.3	349	19	AA683286	Human flt-3 ligand
39	736.5	59.3	523	19	AA678008	Trimeric Flt3L-G-C
40	735	59.2	140	19	AA677911	Human flt-3 ligand
41	735	59.2	140	19	AA69035	Human flt-3 receptor
42	735	59.2	144	19	AA677928	Flt3 ligand FLT4C
43	735	59.2	144	19	AA69052	Human flt-3 receptor
44	735	59.2	313	19	AA683294	Human flt-3 ligand
45	733.5	59.1	286	19	AA683303	Human flt-3 ligand

ALIGNMENTS

RESULT 1
AA67541
ID AAR67541 standard; Protein; 235 AA.
AC AAR67541;
XX
XX 05-AUG-1995 (first entry)
XX Human flt-3 ligand.
XX
XX Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= Sig_peptide
XX /note= "signal peptide may extend to position 27"
XX Domain 27..182
XX /label= "Extracellular domain
XX /note= "Extracellular domain may start at
XX position 28"
XX Domain 183..205
XX /label= Transmembrane_domain
XX Domain 206..235
XX /label= Cytoplasmic_domain
XX
XX EP627487-A.
XX
XX PD 07-DEC-1994.
XX
XX PF 19-MAY-1994; 94EP-0303575.
XX
XX PF 24-MAY-1993; 93US-0068394.
XX

PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX (IMV) IMMUNEX CORP.
 PA Beckmann MP, Lyman SD;
 XX WPI: 1995-008071/02.
 DR N-PSDB; AAQ79079.
 XX Isolated ligands for flt 3 receptors - useful for treating
 PT anaemia, AIDS and various cancers
 PS Disclosure; Page 29-30; 33pp; English.
 XX A human T-cell lambda-gt10 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 XX Sequence 235 AA;
 SQ

Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAWSPPTVLLLLSSGLSGTQCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 DB 1 mtvlapawspptvllllssglsqcsfghspissdfavkirelsdyllqdyptv 60
 QY 61 ASNLDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYVTEIHFTVKCAFQPPPSCL 120
 DB 61 asnldeelcggglwrlvlagrwmrlktvagskmgllervnteihfvtkcafpppscl 120
 QY 121 RFVQTNISRLQETSQVLVAKPWITRONFSRCLELQCPDSTLPPWSPRPLEATPT 180
 DB 121 rfvtqnisrlqetsqvlvawkpwitronfsrclelqcpdstlppwsprrpleatpt 180
 QY 181 ACQPPLLLLLLPVGILLAAWCLHWQTRRRTPRGQVPPVPSPQDLLLVEH 235
 DB 181 apqppllllllpvgillllaaawclhwqtrrrtrtprgqvppvpqpqdllllveh 235

RESULT 2
 ID AAW67769 standard; Protein; 235 AA.
 AC AAW67769;
 XX
 DT 25-MAR-1999 (first entry)
 XX Human flt3-ligand.
 DE
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 OS Homo sapiens.
 XX WO9857655-A1.
 PN
 XX 23-DEC-1998.
 PD
 XX 12-JUN-1998; 98WO-US12085.
 PF
 XX 17-JUN-1997; 97US-0877421.
 PR
 XX (IMV) IMMUNEX CORP.
 PA

XX Abbott NM, Mowat AM, Viney JL;
 PI WPI: 1999-070422/06.
 DR N-PSDB; AAV81506.
 DR
 XX Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 PS Claim 1; Page 14-15; 25pp; English.
 XX A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 XX Sequence 235 AA;
 SQ

Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAWSPPTVLLLLSSGLSGTQCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 DB 1 mtvlapawspptvllllssglsqcsfghspissdfavkirelsdyllqdyptv 60
 QY 61 ASNLDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYVTEIHFTVKCAFQPPPSCL 120
 DB 61 asnldeelcggglwrlvlagrwmrlktvagskmgllervnteihfvtkcafpppscl 120
 * QY 121 RFVQTNISRLQETSQVLVAKPWITRONFSRCLELQCPDSTLPPWSPRPLEATPT 180
 DB 121 rfvtqnisrlqetsqvlvawkpwitronfsrclelqcpdstlppwsprrpleatpt 180
 QY 181 ACQPPLLLLLLPVGILLAAWCLHWQTRRRTPRGQVPPVPSPQDLLLVEH 235
 DB 181 apqppllllllpvgillllaaawclhwqtrrrtrtprgqvppvpqpqdllllveh 235

RESULT 3
 ID AAY69719 standard; Protein; 235 AA.
 XX AAY69719;
 AC AAY69719;
 XX
 DT 05-JUL-2000 (first entry)
 XX Full length wild type human flt-3 protein.
 DE
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX Homo sapiens.
 OS
 XX WO200001823-A2.
 PN
 XX 13-JAN-2000.
 PD

```
XX 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
XX (IMMV) IMMUNEX CORP.
XX Graddis TJ, McGrew JT;
XX WPI; 2000-182115/16.
XX N-PSDB; AAZ59064.
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
XX immune response stimulation or treatment of pathological conditions
XX contains amino acid substitutions at positions 8, 84, 118 or 122.
XX
XX Claim 1; Page 72-73; 90pp; English.
XX
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
XX which exhibits increased or decreased biological activity relative to
XX the full length wild type (this sequence) or mature (AAV69720) flt3-L
XX polypeptides. The flt3-L protein binds cell surface tyrosine kinase
XX receptors and regulate growth and differentiation of hematopoietic
XX progenitor cells. The flt3-L protein can be used to induce cellular
XX expansion (especially in vivo) or differentiation, e.g. in
XX hematopoietic, natural killer (NK) or dendritic cells, especially in the
XX presence of growth factors such as interleukins, colony stimulating
XX factors or protein kinases. The protein can also modulate, augment or
XX enhance a patient's immune response and can be used to treat an immune
XX disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
XX may be used to treat a pathological condition e.g. myelodysplasia,
XX aplastic anemia, HIV infection, breast, small cell lung, testicular or
XX ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
XX leukemia.
XX
XX Sequence 235 AA;
XX
XX Query Match 100.0%; Score 1242; DB 21; Length 235;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-109;
XX Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPYPTV 60
XX Db 1 mtvlapawspttylllllssglsgtqdcfsfhspsissdfavkirelsyllqdpv 60
XX
XX QY 61 ASNLQDEELCGGLWRLVLAQRWMLERLKTAVGSKMOGLLERNVTEHFVTKCAFQPPPSCL 120
XX Db 61 asnlqdeecgglwrlvlagrwmrlktavagskmgllervntelhfvtkcafpppscl 120
XX
XX QY 121 RFVOTNISRLQETSEQLVAKPWITRQNFSCLELCQDPSSTLPWPSPRPLEATAPT 180
XX Db 121 rfvgtnisrllqetseqlvawkpwttrqnfscrlcqlcqdsstlpwp sprpleatapt 180
XX
XX QY 181 APQPPILLLLLPVGLLLAAWCLHWQRTRRRTPRGEQVPVPSPQDLLLVEH 235
XX Db 181 apqppilllllpvglllaawclhwqrtrrrtpргеeqvppspqdlllveh 235
XX
XX RESULT 4
XX AAB20192
XX ID AAB20192 standard; Protein; 235 AA.
XX
XX AC AAB20192;
XX
XX DT 14-MAY-2001 (first entry)
XX
XX DE Human Flt-3 ligand.
XX
XX KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;
XX lymphoma; autoimmune disease; infection; gene therapy.
XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..26
XX FT Protein /label= Signal_peptide
XX FT Protein 27..235
XX FT Domain /label= Mature_protein
XX FT Domain 27..182
XX FT Domain /label= Extracellular_domain
XX FT Domain 183..205
XX FT Domain /label= Transmembrane_domain
XX FT Domain 206..235
XX FT Domain /label= Cytoplasmic_domain
XX
XX PN WO200109303-A2.
XX
XX XX
XX PD 08-FEB-2001.
XX
XX PF 31-JUL-2000; 2000WO-US20679.
XX
XX PR 30-JUL-1999; 99US-0146170.
XX
XX PA (VICA-) VICAL INC.
XX
XX PI Hermanson GG;
XX
XX XX
XX WPI; 2001-123319/13.
XX
XX DR N-PSDB; AAF30310.
XX
XX XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotides, useful for suppressing tumour growth and for treating
XX autoimmune diseases. (e.g. rheumatoid arthritis).
XX
XX PS Claim 2; Page 132-133; 149pp; English.
XX
XX CC The present sequence is that of human Fms-like tyrosine kinase
XX (Flt-3 ligand). The invention is directed to enhancing the
XX immune response of a vertebrate to an antigen or a cytokine by
XX administering in vivo, into a tissue of a vertebrate, a Flt-3
XX ligand-encoding polynucleotide, and 1 or more antigen- or
XX cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
XX polynucleotide may encode the present full-length human Flt-3
XX ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
XX or 27-235 of the ligand. The polynucleotides are incorporated
XX into the cells of the vertebrate in vivo, and a prophylactically
XX or therapeutically effective amount of Flt-3 ligand and 1 or more
XX antigens or cytokines is produced in vivo. Pharmaceutical
XX compositions comprising the polynucleotides are useful for
XX suppressing tumour growth in a mammal. The tumour is melanoma,
XX glioma or lymphoma, particularly B-cell lymphoma. They can also
XX be used for the prophylactic and/or therapeutic treatment of:
XX (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
XX and C in humans), parasitic (e.g. malaria) and fungal infections;
XX (b) autoimmune diseases (e.g. rheumatoid arthritis and
XX osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
XX Various other examples of these diseases are given in the
XX specification.
XX
XX SQ Sequence 235 AA;
XX
XX Query Match 100.0%; Score 1242; DB 22; Length 235;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-109;
XX Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPYPTV 60
XX Db 1 mtvlapawspttylllllssglsgtqdcfsfhspsissdfavkirelsyllqdpv 60
XX
XX QY 61 ASNLQDEELCGGLWRLVLAQRWMLERLKTAVGSKMOGLLERNVTEHFVTKCAFQPPPSCL 120
XX Db 61 asnlqdeecgglwrlvlagrwmrlktavagskmgllervntelhfvtkcafpppscl 120
XX
XX QY 121 RFVOTNISRLQETSEQLVAKPWITRQNFSCLELCQDPSSTLPWPSPRPLEATAPT 180
XX Db 121 rfvgtnisrllqetseqlvawkpwttrqnfscrlcqlcqdsstlpwp sprpleatapt 180
XX
XX QY 181 APQPPILLLLLPVGLLLAAWCLHWQRTRRRTPRGEQVPVPSPQDLLLVEH 235
XX Db 181 apqppilllllpvglllaawclhwqrtrrrtpргеeqvppspqdlllveh 235
XX
XX RESULT 4
XX AAB20192
XX ID AAB20192 standard; Protein; 235 AA.
XX
XX AC AAB20192;
XX
XX DT 14-MAY-2001 (first entry)
XX
XX DE Human Flt-3 ligand.
XX
XX KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
XX immunotherapy; therapy; tumour; cancer; melanoma; glioma;
XX lymphoma; autoimmune disease; infection; gene therapy.
XX
```

AA	SQ	Sequence	235	AA;
		Query Match	99.5%	Score 1236; DB 16; Length 235;
		Best Local Similarity	99.6%	Pred. NO. 1 "3e-108;
		Matches 234; % Conservative	0;	Mismatches 1; Indels 0; Gaps

XX	WO200109303-A2.
PN	
XX	
PD	08-FEB-2001.
XX	
XX	
PF	31-JUL-2000; 2000WO-US20679.
XX	
PR	30-JUL-1999; 99US-0146170.
XX	
PA	(VICA-) VICAL INC.
XX	
PI	Hermanson GG;
XX	
DR	WPI; 2001-123319/13.
DR	N-PSDB; AAF30312.
XX	
XX	Immunogenic compositions comprising Flt-3 ligand encoding
PT	polynucleotide and one or more antigen, or cytokine encoding
PT	polynucleotides, useful for suppressing tumour growth and for treating
PT	autoimmune diseases (e.g. rheumatoid arthritis) -
XX	
XX	Claim 2; Page 137-138; 149pp; English.
XX	
CC	The present sequence is that of human Fms-like tyrosine kinase
CC	(Flt-3 ligand). The invention is directed to enhancing the
CC	immune response of a vertebrate to an antigen or a cytokine by
CC	administering in vivo, into a tissue of a vertebrate, a Flt-3
CC	ligand-encoding polynucleotide, and 1 or more antigen- or

cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and/or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.

XX Sequence 235 AA;

Query Match 99.5%; Score 1236; DB 22; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.3e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLPAWSPTTYLLLLLLSSGSGTQCSFQHSPISSDFAVKIRELSDYLLQDPYPTV 60
Db 1 mtvlpawspttyllllllssgslgtqdcfsqhspsissdfavkirelsdyllqdpv 60

QY 61 ASNLQDEELCGGLRLVLAQRWRLKTVAGSKMGLLRRVNTTEHFVTKCAFQPPSCL 120
Db 61 asnlqdeecgglrllvlaqrwmerlktvagskmqglrrvnttehfvtkcafpppscl 120

QY 121 RFVQTNISRLLOETSEOLVALKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAPT 180
Db 121 rfvtgnisrllqetseqlvalkpwtitronfsrclclqcpdssstlppwsprip 180

QY 181 APQPPLLLLLLPVGLLLAAWCLHWQTRRRTRPRGQGVPPVPSQDILLVEH 235
Db 181 apqppllllllpvglillaaawclhwqtrrrtrprgqgvppvpsqdillveh 235

RESULT 7
AA69721
ID AAY69721 standard; Protein; 212 AA.
AC AAY69721;
DT 05-JUL-2000 (first entry)
DE Human flt-3 mutein L-3H.
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
OS Homo sapiens.
OS Synthetic.
PN WO200001823-A2.
XX 13-JAN-2000.
PD 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
PA (IMV) IMMUNEX CORP.

PI Graddis TJ, McGrew JT;
XX WPI; 2000-182115/16.
DR
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion.
PT Immune response stimulation or treatment of pathological conditions.
PT Contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 4; Page 79-80; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69713) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 212 AA;

Query Match 90.5%; Score 1124; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.2e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SCTQDCSFQHSPISSDFAVKIRELSDYLLQDPYPTVNASLQDEELCGGLRLVLAQRWME 84
Db 2 sctqdcfsqhspsissdfavkirelsdyllqdpvptvasnlqdeecgglrllvlaqrwme 61

QY 85 RLKTVAGSKMGLLRRVNTTEHFVTKCAFQPPSPSCIRFVQTNISRLLOETSEOLVALKPW 144
Db 62 rlktvagskmqglrrvnttehfvtkcafpppsclrfvtgnisrllqetseqlvalkp 121

QY 145 ITRQNFSCLELQCPDSSSTLPPWSPRPLEATAPTAPQPPLLLLLLPVGLLLAAWCL 204
Db 122 itrqnfsrclclqcpdssstlppwsprip 181

QY 205 LHWQTRRRTRPRGQGVPPVPSQDILLVEH 235
Db 182 lhwqtrrrtrprgqgvppvpsqdillveh 212

RESULT 8
AAW69007
ID AAW69007 standard; peptide; 209 AA.
XX
AC AAW69007;
XX
DT 01-OCT-1998 (first entry)
DE Human flt-3 receptor agonist.
XX
KW Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer; bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection; congenital metabolic disease; neurological disease; therapy; dendritic cell production.
XX
OS Homo sapiens.
XX
PN WO9818923-A1.
XX
PD 07-MAY-1998.

XX 23-OCT-1997; 97WO-US18700.
XX
XX
XX 25-OCT-1996; 96US-0030094.
XX
XX
XX (SEAR) SEARLE & CO G D.
XX
XX Feng Y, McKearn JP, McWherter CA, Minnerly JC, Minster NI;
XX Staten NR, Streeter PR, Woulfe SL;
XX WPI; 1998-272218/24.
XX
XX Rearranged flt-3 receptor agonists and nucleic acids encoding them -
XX used to stimulate production of haematopoietic and dendritic cells,
XX for treatment of haematological diseases, bone marrow reconstitution
XX and in gene therapy
XX
XX Disclosure; Page 9-10; 158pp; English.
XX
XX This sequence represents a rearranged human flt-3 receptor agonists of
XX the invention. The agonists have a modified flt-3 ligand amino acid
XX sequence. The agonists are used to stimulate production of haematopoietic
XX cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
XX expansion for subsequent transplantation, e.g. to reconstitute bone
XX marrow after chemotherapy, disease etc., or to treat haematological
XX disease such as drug-induced myelosuppression, defects caused by
XX infections, burns or renal dialysis. Optionally ex vivo expanded cells
XX are transduced with a gene therapy vector for treating e.g. congenital
XX metabolic diseases, immune deficiency, neurological disease, cancer and
XX infections. The agonists can also be used in the treatment of tumours,
XX infections and autoimmune disease, when administered optionally with an
XX antigen. The agonist can also be used in the production of dendritic
XX cells for use as an immunising adjuvant for treatment disorders including
XX acquired immune deficiency syndrome. Compared with native ligands, the
XX new agonists have better stimulatory activity, reduced side effects
XX and/or better physical properties such as solubility, stability or refold
XX efficiency. When used together with other stimulatory agents, the
XX agonists provide a synergistic effect.
XX
XX Sequence 209 AA;

Query Match 89.7%; Score 1114; DB 19; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.6e-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDQCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDEELCGGLRLVLAQRWMLR 86
DB 1 tqdcsfqhspsissdfavkirelsylylqdyptvasnlqdeelcggglrwlvlqqrwmerl 60
QY 87 KTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWIT 146
DB 61 ktvagskmqgllervntehfvtkcafpppsclrfvqtnisrllqetseqvlakpwit 120
QY 147 RQNFSCRLELQCPDSTLPPWSPRPLEATAPQPPILLLLLPVGLLLAAWCLH 206
DB 121 rqnfsrcllelqcpdstlppwsprrpleatapqppllllllpvglillaaawclh 180
QY 207 WQTRRTTRPRGEGVPPVPSQDILLVEH 235
DB 181 wqtrrttrprgeqvppvpsqdillveh 209

RESULT 9

ID AAY69720
AC AAY69720 standard; Protein; 209 AA.

XX AAY69720;

XX
XX 05-JUL-2000 (first entry)

DE Mature wild type human flt-3 protein.

XX

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia.
XX Homo sapiens.
XX OS
XX WO200001823-A2.
XX
XX 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Graddis TJ, McGrew JT;
XX
XX WPI; 2000-182115/16.
XX N-PSDB; AAZ59064.
XX
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
XX immune response stimulation or treatment of pathological conditions
XX contains amino acid substitutions at positions 8, 84, 118 or 122 .
XX
XX Claim 1; Page 89-90; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
XX which exhibits increased or decreased biological activity relative to
XX the full length wild type (AAV69719) or mature (this sequence) flt3-L
XX polypeptides. The flt3-L protein binds cell surface tyrosine kinase
XX receptors and regulate growth and differentiation of hematopoietic
XX progenitor cells. The flt3-L protein can be used to induce cellular
XX expansion (especially in vivo) or differentiation, e.g. in
XX hematopoietic, natural killer (NK) or dendritic cells, especially in the
XX presence of growth factors such as interleukins, colony stimulating
XX factors or protein kinases. The protein can also modulate, augment or
XX enhance a patient's immune response and can be used to treat an immune
XX disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
XX may be used to treat a pathological condition e.g. myelodysplasia,
XX aplastic anemia, HIV infection, breast, small cell lung, testicular or
XX ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
XX leukemia.

XX Sequence 209 AA;

Query Match 89.7%; Score 1114; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.6e-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDQCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDEELCGGLRLVLAQRWMLR 86
DB 1 tqdcsfqhspsissdfavkirelsylylqdyptvasnlqdeelcggglrwlvlqqrwmerl 60
QY 87 KTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWIT 146
DB 61 ktvagskmqgllervntehfvtkcafpppsclrfvqtnisrllqetseqvlakpwit 120
QY 147 RQNFSCRLELQCPDSTLPPWSPRPLEATAPQPPILLLLLPVGLLLAAWCLH 206
DB 121 rqnfsrcllelqcpdstlppwsprrpleatapqppllllllpvglillaaawclh 180
QY 207 WQTRRTTRPRGEGVPPVPSQDILLVEH 235
DB 181 wqtrrttrprgeqvppvpsqdillveh 209

RESULT 10

AAV69723
ID AAY69723 standard; Protein; 209 AA.
AC AAY69723;
DT 05-JUL-2000 (first entry)
DE Human flt-3 mutein K84E.
DE
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI; 2000-182115/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 4; Page 84-85; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA;
Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 27 TQCSFQHSPISSFAVKIRELSYLLQDYPTVTVASNLQDEELGGLRWLRVLAQRWMERL 86
DB 1 tqdcsfghspissafavkirelsydlldyptvtvasnlqdeecgglwrlvlagrwrmerl 60
QY 87 KTVAGSKMGILLERVNTEIHVFVKCAFPQPPSCILRFVOTNISRLLQETSEQLVAKPWIT 146
DB 61 ktvagskmgillervnteihtvtecatqpppsclrfvgtvnlsrllqetseqlvakpwit 120

QY 147 RQNFRCLEQOCQDSSLTLPWPSPRLEATAPQPPILLILLPVGILLIAAACLH 206
DB 121 rqnfsrclqcdpsdstlppwsprrleatpqppllllllpvglllaaawclh 180
QY 207 WQTRRTPRPGEQVPPVPSQDILLVEH 235
DB 181 wqtrrtprpgeqvppvpsqdillveh 209

RESULT 11
ID AAY69726
AC AAY69726 standard; Protein; 209 AA.
XX
AC AAY69726;
XX
DT 05-JUL-2000 (first entry)
DE Human flt3 mutein Q122R.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI; 2000-182115/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 4; Page 88-89; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA;
Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;

Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDGCSFQHSPISSDFAYKIRELSYLLQDPYPTVASNLQDEELCGGLWRLVLAQRWMLR 86
 Db 1 tqdcsfghspissdfavkirelsdyllqdpvtvasnlqdeecgglwrlvlaqrwmlr 60

QY 87 KTVAGSKMGGLLERVTNTEIHFTVKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 ktvagskmqgllervntelhfvtkcafpppsclrfvqtnisrllqetseqlvalkpwt 120

QY 147 RQNFSCRLELCQCPDSSLPPWSPRPLEATAPTAPQPPILLLLLLPVGILLAAACWLH 206
 Db 121 rnfscrlelcqcpdssstlppwspripieataptapqppllllllpvgillaaaacwlh 180

QY 207 WQTRRTTRPRGQVPPVPSQDILLVEH 235
 Db 181 wqtrrttrprgqvpvpspqdillveh 209

RESULT 12
 AAY69727
 ID AAY69727 standard; Protein; 209 AA.
 AC AAY69727;
 XX
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutein L36F.
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 13; Page 82-83; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or

CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX Sequence 209 AA;

Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TDGCSFQHSPISSDFAYKIRELSYLLQDPYPTVASNLQDEELCGGLWRLVLAQRWMLR 86
 Db 1 tqdcsfghspissdfavkirelsdyllqdpvtvasnlqdeecgglwrlvlaqrwmlr 60

QY 87 KTVAGSKMGGLLERVTNTEIHFTVKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 ktvagskmqgllervntelhfvtkcafpppsclrfvqtnisrllqetseqlvalkpwt 120

QY 147 RQNFSCRLELCQCPDSSLPPWSPRPLEATAPTAPQPPILLLLLLPVGILLAAACWLH 206
 Db 121 rnfscrlelcqcpdssstlppwspripieataptapqppllllllpvgillaaaacwlh 180

QY 207 WQTRRTTRPRGQVPPVPSQDILLVEH 235
 Db 181 wqtrrttrprgqvpvpspqdillveh 209

RESULT 13
 AAY69729
 ID AAY69729 standard; Protein; 209 AA.
 XX AAY69729;
 AC AAY69729;
 XX
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutein A64T.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 13; Page 78-79; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L

CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L26F mutant polypeptide. The flt-3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt-3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX Sequence 209 AA;

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 27 TDGCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDELCGLRLVLAQRWMLR 86
Db 1 tqdcfsfqpissdfavkirelsdyllqdyptvasnlqdeecgglwrlvlagrwmrl 60
QY 87 KTVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 146
Db 61 ktvtgskmgllervnteihfvtkcafpqppscrlfvqtnisrlqetseqvllkpwt 120
QY 147 RQNFRCLELQCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPVGLLLAAAWCLH 206
Db 121 rqnfrsclclqcpdssstlppwsprrpleataptapqppllllllpvglllaaawclh 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 wqtrrrtrprgeqvppvpsqdillveh 209

RESULT 14
AY69722
ID AAY69722 standard; Protein; 209 AA.
XX AC AAY69722;
XX 05-JUL-2000 (first entry)
XX Human flt-3 mutein H8Y.
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX Homo sapiens.
OS Synthetic.
XX WO200001823-A2.
XX 13-JAN-2000.
XX 25-JUN-1999; 99WO-US14296.
XX 02-JUL-1998; 98US-0109100.
XX (IMV) IMMUNEX CORP.
XX Graddis TJ, McGrew JT,
XX WPI; 2000-182115/16.

XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 .
XX Claim 4; Page 81-82; 90pp; English.
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the H8Y mutant polypeptide. The flt-3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt-3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.3e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 27 TDGCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDELCGLRLVLAQRWMLR 86
Db 1 tqdcfsfqpissdfavkirelsdyllqdyptvasnlqdeecgglwrlvlagrwmrl 60
QY 87 KTVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWIT 146
Db 61 ktvtgskmgllervnteihfvtkcafpqppscrlfvqtnisrlqetseqvllkpwt 120
QY 147 RQNFRCLELQCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPVGLLLAAAWCLH 206
Db 121 rqnfrsclclqcpdssstlppwsprrpleataptapqppllllllpvglllaaawclh 180
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
Db 181 wqtrrrtrprgeqvppvpsqdillveh 209

RESULT 15
AY69724
ID AAY69724 standard; Protein; 209 AA.
XX AC AAY69724;
XX 05-JUL-2000 (first entry)
XX Human flt-3 mutein K84T.
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX Homo sapiens.
OS Synthetic.
XX WO200001823-A2.
XX 13-JAN-2000.

XX 25-JUN-1999; 99WO-US14296.
 XX 02-JUL-1998; 98US-0109100.
 XX (IMMV) IMMUNEX CORP.
 XX Graddis TJ, McGrew JT;
 XX WPI; 2000-182115/16.
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 XX immune response stimulation or treatment of pathological conditions
 XX contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 XX Claim 4; Page 85-86; 90pp; English.
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 XX which exhibits increased or decreased biological activity relative to
 XX the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 XX polypeptides. This sequence represents an example of the novel flt-3
 XX ligands and comprises the K84T mutant polypeptide. The flt3-L protein
 XX binds cell surface tyrosine kinase receptors and regulate growth and
 XX differentiation of hematopoietic progenitor cells. The flt3-L protein can
 XX be used to induce cellular expansion (especially in vivo) or
 XX differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 XX cells, especially in the presence of growth factors such as interleukins,
 XX colony stimulating factors or protein kinases. The protein can also
 XX modulate, augment or enhance a patient's immune response and can be used
 XX to treat an immune disorder (e.g. allergy, autoimmunity or
 XX immunosuppression). The protein may be used to treat a pathological
 XX condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 XX small cell lung, testicular or ovarian cancer, lymphoma, multiple
 XX myeloma, neuroblastoma or acute leukemia.
 XX Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.3e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 27 TDGCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRMERL 86
 Db 1 tqdcsfqhspsissdfavkirelsdylldqypvtvasnlqdeecgglwrlvlaqrwmerl 60
 Qy 87 KTVAGSKMOGLLERVNTIEHFVTKAFOPPPSCLEFVOTNISRLLOETSEQLVALKPWIT 146
 Db 61 ktvagskmgglleervnteihtvtcafpqppscrlfvdqtnisrlldetseqvlalkpwit 120
 Qy 147 RNFSTRCLQLQCPDSSTLPPPPSPRPLEATAPAPQPLLLLLPVGLLLAAACLIH 206
 Db 121 rnfstrclqlcqpdssstlppppsprpleataptapqppllllllpvglillaaawclh 180
 Qy 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
 Db 181 wqtrrrtprrgeqvppvpsqdillveh.209

Search completed: April 1, 2002, 06:18:09
 Job time: 255 sec

Access DB# 63508

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
 CM1 1E07 - 703-308-4498
 jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>4/1/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>4/1/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>60</u>	Other _____	Other (specify) _____

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 68.03 seconds
(without alignments)
263.134 Million cell updates/sec

Title: US-08-162-407-6
Perfect score: 1242
Sequence: 1 MTVLAPAWSPTTYLLLLLLL.....RPGQVPPVPQDILLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	89.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	Flt3 ligand altern
4	768.5	61.9	231	2 A49265	flt3/flk-2 ligand
5	605.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	605.5	48.8	220	2 I38343	flt3 ligand isofo
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 T3BE12	74K alpha trans-in
9	89.5	7.2	474	2 T19543	hypothetical prote
10	89	7.2	387	2 I48201	adhalin - golden h
11	89	7.2	793	1 S60735	splicing factor SF
12	88.5	7.1	1386	2 T00257	hypothetical prote
13	88	7.1	753	2 J00532	Op protein - Kenne
14	87.5	7.0	479	1 A32290	protein-tyrosine-p
15	87	7.0	910	2 A53137	tyrosine kinase re
16	86.5	7.0	590	2 A40437	glutamic acid-rich
17	86	6.9	299	2 T17832	hypothetical prote
18	86	6.9	485	2 A33647	hypothetical prote
19	86	6.9	746	2 T28004	sulfated surface g
20	85	6.8	366	2 A37374	hypothetical prote
21	84	6.8	263	2 T03162	Fc gamma (IgG) rec
22	84	6.8	757	2 A39283	segment protein 6
23	83.5	6.7	199	2 E75630	gamma-glutamyl car
24	83.5	6.7	530	2 A45690	hypothetical prote
25	83	6.7	1509	2 T19486	transactivator EBN
26	82.5	6.6	418	2 T19800	hypothetical prote
27	82.5	6.6	426	2 I36948	Ig epsilon-chain
28	82.5	6.6	512	2 D40829	activin receptor 1
29	82.5	6.6	513	2 J01484	activin receptor p

30 82 6.6 106 2 T06479 proline/leucine-ri
31 82 6.6 854 2 T23837 hypothetical prote
32 81.5 6.6 485 2 C75460 hypothetical prote
33 81.5 6.6 488 2 S13423 stromelysin 3 (EC
34 81.5 6.6 958 2 T13593 hypothetical prote
35 81.5 6.6 1119 2 T50995 related to cytoske
36 81 6.5 196 2 B48232 cysteine-rich exte
37 81 6.5 209 2 A48232 cysteine-rich exte
38 81 6.5 388 2 T15591 probable transposa
39 81 6.5 428 1 EHHU Ig epsilon chain C
40 80.5 6.5 636 2 JW0047 class I cyto kinase
41 80.5 6.5 1176 2 T49482 hypothetical prote
42 80.5 6.5 1305 2 T13592 hypothetical prote
43 80.5 6.5 1402 2 T46707 translocation initia
44 80 6.4 398 2 T52311 isopenicillin N ep
45 80 6.4 434 2 S74706 (S)-2-hydroxy-acid

ALIGNMENTS

RESULT 1

I38440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Down
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor f
A:Reference number: I38440; MUID:94235842,
A:Accession: I38440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AAAL98251.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1163-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RE2>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AAA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotni
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', 73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAAL17999.1; PID:9483845
A:Note: the authors translated the codon AGT for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSFSSDFAVKIRELSDFLLQDYPVT 60
|||||
Db 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSFSSDFAVKIRELSDFLLQDYPVT 60
|||||
QY 61 ASNLDEELCGGLRWLRVLAQWRMERLKTAVAGSKMQGLLERVNTIEHVTKCAFPPPSCL 120
|||||
Db 61 ASNLDEELCGGLRWLRVLAQWRMERLKTAVAGSKMQGLLERVNTIEHVTKCAFPPPSCL 120
|||||
QY 121 RFVQTNISRLQETSETSQLVALKPWITRQNFSCRLELCQCPDSSLTLPFPWSPRPLEATPT 180

Db 121 RFVQTNISRLLOETSEQLVALKPWITRQNFSCLELQCPDSDSTLPPWSPRPLEATPT 180
 QY 181 APQPLLLLLLPVGLLLAAWCLHWQTRRRTPRPGEQVPPVSPQDLLLLVEH 235
 Db 181 APQPLLLLLLPVGLLLAAWCLHWQTRRRTPRPGEQVPPVSPQDLLLLVEH 235
 RESULT 2
 S43293
 FLT3/FLK2 ligand (clone S109) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43293
 R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.; Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43293
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-245 <HAN>
 A>Note: the authors translated the codon AGT for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;
 Best Local Similarity 73.0%; Pred. No. 8.5e-67;
 Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MTVLAPAWSPPTLYLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 Db 1 MTVLAPAWSPPTLYLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRQNFSCLELQCPDSDSTLPPWSPRPLEATPT 180
 Db 121 RFVQTNISRLLOETSEQLVALKPWITRQNFSCLELQCPDSDSTLPPWSPRPLEATPT 180
 QY 181 APQP-----PLLLLLLPVGLLLAAWCLHWQTRRRTPRPGEQVPPVSP 227
 Db 178 WRPHPGDETEAHRGESP-----ARGCIATWQTKLARGSLPWAPLIPSP 222
 QY 228 Q 228
 Db 223 E 223

RESULT 3
 I39076
 Flt3 ligand alternatively spliced isoform - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I39076
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.; Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581
 A:Accession: I39076
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-178 <RES>
 A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
 C:Genetics:
 A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 2.4e-64;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTLYLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 Db 1 MTVLAPAWSPPTLYLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRQNFSCLELQCP 160
 Db 121 RFVQTNISRLLOETSEQLVALKPWITRQNFSCLELQCP 160
 RESULT 4
 A49265
 flt3/flk-2 ligand precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
 C:Accession: A49265; I49347; I49346; S43290
 R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Hollt, D.; Williams, D.E.; Beckmann, M.P.; Cell 75, 1157-1167, 1993
 A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a cDNA
 A:Reference number: A49265; MUID:94084791
 A:Accession: A49265
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-231 <LYM>
 A:Cross-references: GB:L23636; NID:9439441; PIDN:AAA9436.1; PID:g439442
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.; Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581
 A:Accession: I49347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-163, 'G', '165', 'HYAG' <RES>
 A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
 A:Accession: I49346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-197, 'L', 198-231 <RE2>
 A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
 R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.; Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43290
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-197, 'L', 198-231 <HAN>
 A:Experimental source: clone T110
 A>Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
 C:Genetics:
 A:Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
 C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;
 Best Local Similarity 70.3%; Pred. No. 1.3e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAWSPPTLYLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFESHSPISNFVKVFKRELTHLLKDPVT 60
 QY 60 VASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 119
 Db 61 VAVNLQDEKCHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTVTEHFVTSCTFQLPECL 120
 QY 120 LRFVQTNISRLLOETSEQLVALKPWITR--QNFSCLELQCPDSDSTLPPWSPRPLEAT 177

Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQCPDSSTLLPFRSPALEAT 180
 QY 178 APTAQQP--LILLLLLPVGLLLAAAWCLHWQTRRRTPRGEQVPPVPSP 227
 Db 181 ELPEPRPQLLLLLLLPLTLVLLAAWGLRWQRARR--GELHPGVPLP 228

RESULT 5

S43291
 FLT3/FLK2 ligand (clone T118) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43291
 R:Hannum, C.; Cuipepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kasper, A.; Muench, M.; Kelnner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnick, A.
 Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43291
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <HAN>

Query Match 48.8%; Score 606.5; DB 2; Length 220;
 Best Local Similarity 61.5%; Pred. No. 9.4e-45;
 Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAWSP-TTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFVKVRELTDHLKDYPT 60

QY 60 VASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLVRVTEIHFVTKCAFPQPPSC 119
 Db 61 VAVNLQDEKCKALWSLFLAQRWTEIHFVTKCAFPQPPSC 120

QY 120 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQCPDSSTLLPFRSP 173
 Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQCPGNG-----GPRAGHG 174

QY 174 ---LEATAPTAPOPPLLL-----LLLLPVGLLLAA 201

Db 175 ATRLTATALLTVCPLGLLLPLVGTSHMFFLPFLSLSS 212

RESULT 6

I58343
 flt3 ligand isoform 5H - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I58343
 R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K.
 Oncogene 10, 149-157, 1995
 A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand
 A:Reference number: I58343; MUID:95124710
 A:Accession: I58343
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: GB:S76459; NID:9913479; PIDN:AAB33069.1; PID:9913480

Query Match 48.8%; Score 606.5; DB 2; Length 220;
 Best Local Similarity 61.5%; Pred. No. 9.4e-45;
 Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAWSP-TTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFVKVRELTDHLKDYPT 60

QY 60 VASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLVRVTEIHFVTKCAFPQPPSC 119
 Db 61 VAVNLQDEKCKALWSLFLAQRWTEIHFVTKCAFPQPPSC 120

Db 61 VAVNLQDEKCKALWSLFLAQRWIEQLKTVAGSKMQLLEDVTEIHFVTSCTFQPLPEC 120
 QY 120 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQCPDSSTLLPFRSP 173
 Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQCPGNG-----GPRAGHG 174
 QY 174 ---LEATAPTAPOPPLLL-----LLLLPVGLLLAA 201
 Db 175 ATRLTATALLTVCPLGLLLPLVGTSHMFFLPFLSLSS 212

RESULT 7

T22672
 hypothetical protein F54F12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22672
 R:Barlow, K.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19597
 A:Accession: T22672
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1217 <WIL>
 A:Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:F412
 A:Experimental source: clone F54F12
 C:Genetics:
 A:Gene: CESP:F54F12.1
 A:Map position: 3
 A:Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

Query Match 7.5%; Score 93; DB 2; Length 1217;
 Best Local Similarity 23.6%; Pred. No. 6.2;
 Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERLKTAVAGSKMGL---LERVNTIHFVTKCAFPQPPSCLRFPVQTNISRLQETSEQLV 139
 Db 627 MDVAVKAVDGTYSVIDALEKLSTMDLDFQYKFKFAPATLKAMDL----FFASVSNLA 682

QY 140 ALKPWITRQNFSCLEVCQCPDSSTL---PPWSPRPLEATAPAP-----QPPLLLLL 191
 Db 683 ALRPQTTSDTAAPVPIPNKGLNGSPSPPLPPVASSTPAATPESNMILLYII 742

QY 192 LPVGLLLAA-----AWCLHWQTRRRTPRGEQVPPVPSP 227
 Db 743 GAVGGLLVVAITGVILFEVFFQKKKKEDKDD--PPAPLP 781

RESULT 8

TNBE12
 74K alpha trans-inducing protein - human herpesvirus 3
 C:Species: human herpesvirus 3, varicella-zoster virus
 C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
 C:Accession: C27342
 R:Davidson, A.J.; Scott, J.E.
 J. gen. Virol. 67, 1759-1816, 1986
 A:Title: The complete DNA sequence of varicella-zoster virus.
 A:Reference number: A27345; MUID:86306657
 A:Accession: C27342
 A:Molecule type: DNA
 A:Residues: 1-661 <DAV>
 A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001
 C:Genetics:
 A:Gene: 12
 C:Superfamily: herpesvirus 77K alpha trans-inducing protein
 C:Keywords: trans-inducing protein; transcription regulation

Query Match 7.4%; Score 92; DB 1; Length 661;
 Best Local Similarity 26.6%; Pred. No. 3.8;
 Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

```

19  LLSSGLSGTQDCS-----FOHSPFISSDFAVKI--RELUSDYLLQDYPVTVASNLQDEELCG- 71
Db  79  LTFPVQLQSTHERHSHVLLGLHHNNVPESLVVTSMSNDVHDFGMQYMETIQRCILDDLLKLSGD 138
QY  72  GLNRLVLAQRMERLKTVAGSKMOGLLRVN-----TEHFVTKCAFOP---PPSCLRFV 123
Db  139  GLN-WYENTYQWYLYKTTGAEPVTVSEKVNKSKSTVLLFSSVVANKPISRHPFKSKI 197
QY  124  QTNISRLQETTSQVLVAKPWITRONFHSRCLELQCPQDSSTLPPWPSP-RPLEATAPTAP 182
Db  198  NSDYRGICQELREALGAVOKYM---YFMR-----PDDPTNPSPDTRIRVQEIYAATAT 247
QY  183  QPFLLLLLLLPVGLLLLAACWLHMQTRRRTRPRCEQVPPVPSQDLL 231
Db  248  GYGWMLFLLDVVD-----ARVCRHLKLFRRIRGRASV-----IPDILL 287

RESULT      9
T19543
hypothetical protein C28D4.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R/Accession: T19543
R/McMurray, A.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19139
A/Accession: T19543
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-474 CWIL>
A/Cross-references: EMBL:Z82259; PIDN: CAB05139.1; GSPDB: GNO0022; CESP: C28D4
A/Experimental source: clone C28D4
C/Genetics:
A/Gene: CESP:C28D4.2
A/Map position: 4
A/Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/2

```

Query Match	7.2%	Score 89.5;	DB 2;	Length 474;
Best Local Similarity	24.1%;	Pred. No. 4.2;		
Matches	59;	Conservative	29;	Mismatches 82; Indels 75; Gaps 15;
QY	27	TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDPYTVVASNLDQDEELCGGLWRL	76	
Db	65	TTDCVDLKKYFSKFDSSAPISGEILFRARFLCAYL-----GGAWRK	106	
QY	77	VLAQRMMERLKTVAGSKMOGLLERNVTEIHFVYKCAFPQPPSCLR-FVQTNISRLLOET-	134	
Db	107	VKIEEF--RIRATGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIGLLSES	162	
QY	135	-----SEQLVALKPWITQNFSCLELOC-----QPDSSTLPPWPSPR--PLSATA	178	
Db	163	VFTLLSERNLGPKNLGVFGGRPEOFTPSRALQCLELSKPGLSKLIAPYARVHTLDAP	222	
QY	179	PTAQPPLLLLLLPVGLLLAAAWLHWORTRRTP-----RPGE-----QVPEVPSPQD	229	
Db	223	PKSPQ-----TLQTAQWLRE-----KKTAGERPIEMYLTAQVPKSDYPST	266	
QY	230	LLIVE	234	
Db	267	ITVAQ	271	

RESULT 10
I48201
adhalin - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
C:Accession: I48201
R:Roberts, S.L.; Campbell, K.P.
FES Lett. 304, 245-249, 1995
A:Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.
A:Reference number: I48201; MUID:95278335

A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U21677; NID:g726481; PID:g726482
C;Superfamily: mouse adhalin

Query Match 7.2% Score 89; DB 2; Length 387;
Best Local Similarity 23.4%; Pred. No. 3.7;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY	11	TTVLLLLLLSSGLSTQDCSFHSDFAVKIRELSYLLQDYPVTVAASNLQDEELC	70
Db	115	TTTQRLILLI-----EDPEGRPLPYQAEEFLVRSHDVEVL-----PSTPANRFL--TAL	161
QY	71	GGWLRL-----VLAQRWMLRKTVAKSKMOGLLERVNTETIHFVT-----K	110
Db	162	GGUWELGELQLLNTSALDRGGGRVPLPIEGRKEGVYIKVGSATPFSTCLUKWASPD	221
QY	111	CAFOPPP--SC-----LRFVOTNLSRLLOETSEOLVALKPWITQNSRCLELQOCPD	161
Db	222	CAOGQPPLSCYDSLAPHFRVDMCNVSLVDKSVPEPLD-----EVTPTGD	266
QY	162	SSTLPPWPSPRPLEAT-----APTAPOPPLLLLLLPVGLILLAAAMC-----	204
Db	267	GILEHDPPFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGOLKRD	323
QY	205	-----LHWQRTTRRTTRP-----GSEQVPP--VPSP--DLL	231
Db	324	MATSDIOMVHCTIHGNTBELROMAARREVPRPLSTLPWFNVRTGERLPFRVDSAQVPLI	383
QY	232	LVEH	235
Db	384	LDQH	387

RESULT 11
S60735
splicing factor SF3a 120K chain - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S60735; S60733
R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.
RNA 1, 260-272, 1995
A:Title: Mammalian splicing factor SF3a120 represents a new member of the SURP family
A:Reference number: S60733; MUID: 96079558
A:Accession: S60735
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-793 <KRA>
A:Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298
A:Accession: S60733
A:Molecule type: protein
A:Residues: 51-62;82-94;270-275;397-414;448-463 <KRA2>
C:Genetics:
A:Gene: GDB:SF3A120; PRP21; SAP114
A:Cross-references: GDB:9955873
A:Map position: 22q12.1-22qter
C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology
C:Keywords: pre-mRNA splicing
F:714-790/Domain: ubiquitin homology <UBH>

```

Query Match      7.2%; Score 89; DB 1; Length 793;
Best Local Similarity 22.3%; Pred. No. 8.4;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY   4 LAPAWPTTYLLLLLLSGLSGTCQCSFQHSPISSDFAVKIRELSYLLQDPVTVASN 63
    |||I|||
DB   401 LPPAPADPEYL-----SPITGE--KI-----PASK 424

QY   64 LDDEELCGGLRWLRVLQAQWME-RLKTV-----AGSKMQGLLVRNTEIHF 107
```

Db 425 MOEHRIG-----LDPRWLEQRDRSIREKQSDDEVYAPGLDISSKOLAER-RTDIFG 478
Qy 108 VTKA-----FQPPSCCLRF-----VOTNISRLQETSEQLVAKPWI 145
Db 479 VEETAIGKIGEEETKPEKVTWGHSGSMARTQAQANIT--LQEQIEAIHKAGLV 536
Qy 146 ----TRQNF--SRCLELOCQ-----DSSTLP-----PWSRPLEAT-----APT 180
Db 537 PEDDTKERIGSKNEIQPPPPSSAVNIPSSAPITSVPRPTMPPVPRITVVSAVPV 596
Qy 181 APOPELLLLLPVGLLLAAWCLHWQTR-----RRTPRGQVPP-----VPSP 227
Db 597 MPRPPMASVVRLLPGSVIAPMPPIIHAPRINVVMPSPAPPIMAPRPPMIVPTAFVPAP 656
RESULT 12
T00257
hypothetical protein KIAA0476 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00257
R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4: 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: 214085; MUID:98116662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1386 <SEK>
A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1; PID:g3413914
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0476

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
Best Local Similarity 23.1%; Pred. No. 17;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;
Qy 21 SSGLSGTQDCSFQHSPISSDFAVIRELSVDYLLQDYPVTVASNLQDELC---GGLWRL 76
Db 1104 SAGASGKDAPVCGP-----GVLSDRRUCLA--LDEPOLCNGHMGASRR 1148
Qy 77 VLAQRWMLKTVAGSKMGLLERNVTEIFVTKAFQPPSPCLRFVOTNISRLQETSE 136
Db 1149 VESGAWAYLSPLVRKELESVNEGSEV-----LALPELPSAHPIIFWNLLWYFQRL-- 1201
Qy 137 OLVALKPWITRQNSRCLELOCQ-PDSSTLPPW-SPRPLEA-----TAPTAPQPP 185
Db 1202 RUPSILPGLVAS-----CDGSPSHSQAPSPWLTDPASVQVRLMDVLTDPDPSNCP 1253
Qy 186 LLLLLLPVGLLLAAWCLHWQTRRRTPRGQVPPVPSQDILLVE 234
Db 1254 LYVL-----WRVHSQ-IPORVWMPG-----PVPASLSLALLE 1284

RESULT 13
JQ0532
OP protein - Kennedy's yellow mosaic virus
C:Species: Kennedy's yellow mosaic virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C:Accession: JQ0532
R:Ding, S.; Keese, A.
J. Gen. Virol. 71, 925-931, 1990
A:Title: The nucleotide sequence of the genomic RNA of Kennedy's yellow mosaic tymovirus-
A:Reference number: JQ0532; MUID:90218040
A:Accession: JQ0532
A:Molecule type: mRNA
A:Residues: 1-753 <DN>
A:Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; PID:d1000986; PID:g221970
A:Experimental source: strain Jervis Bay isolate

Query Match 7.1%; Score 88; DB 2; Length 753;
Best Local Similarity 22.3%; Pred. No. 9.6;
Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;
Qy 100 RVNTEIFVTKAFQPPSPCLRF-----VQTNIS-----RLQETSEQLVAKPWITR 147
Db 420 RLSTQPPSPQTSSTSSPPSPRTDASCIQIPLASPPSKREKSLPHFSHQ-----PPSHSK 475
Qy 148 ONFSR-----CLEQOCQDSSTLPPSPRPLEATAPAPQPLLLLLLP----- 193
Db 476 RNLRRHSALPLLLPIHPTKTQHPAPVQP--TAGPTPHPPPTKKIPLHPPKSOERHPS 533
Qy 194 -----VGLLLAAACLHWQTRRRTPRGQVPPVPS 226
Db 534 PPDVFHDCQPSSTSHVGYRLLGSGISLPFLAFW-----RRRSPNPARHLPPPPP 586
Qy 227 PQDLW230
Db 587 PRKL 590

RESULT 14
A32290
protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila)
C:Species: Drosophila melanogaster
C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C:Accession: A32290; SI2008
R:Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
A:Title: Genetic control of cell division patterns in the Drosophila embryo.
A:Reference number: A32290; MUID:89195217
A:Accession: A32290
A:Molecule type: mRNA
A:Residues: 1-479 <EDG>
A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
EMBO J. 9, 3565-3571, 1990
A:Title: Complementation of fission yeast cdc2(ts) and cdc25(ts) mutants identifies
A:Reference number: SI2008; MUID:91006056
A:Accession: SI2008
A:Molecule type: mRNA
A:Residues: 1-227 'A', 229-479 <JIM>
A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707
C:Genetics:
A:Gene: FlyBase:stg
A:Cross-references: FlyBase:FBgn0003525
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine
A:Pathway: initiation of mitosis
A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphatase
C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolysis
F:252-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PPP>
F:379/Active site: Cys (phosphocysteine intermediate) #status predicted
F:385/Binding site: substrate phosphate (Arg) #status predicted

Query Match 7.0%; Score 87.5; DB 1; Length 479;
Best Local Similarity 22.9%; Pred. No. 6.3;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
Qy 1 MTVLAPAPSPPTTYLL---LLLSGLSTQDCSFQHSPISSDFAVIRELSYLLQDYP 57
Db 72 MGLSPESGFQFVVRQPKILPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
Qy 58 VTVASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIFVTKAFQPP 117
Db 118 CSMESMDDE-----TWLEFEMESQSQ-----QTALGF-----P 146
Qy 118 SCLRFVOTNISRLQETSEQLVAKP---WITRQNFSCRLEL-QCQPDSTLPPWSPRP 173
Db 147 SGLN-----SLISQIKQPAKSPAGLSMRPVSRRCLSWTESNTSTTTTPPKTPE- 199

Qy 174 LEATAPTA---PQPLL LLLLLLVGL LLLAAAWCLHWQRTTRTPRGEQVPPVPSQDL 230
|||
Db 200 ---TARDCFKRPEPP-----ASANGSPIQSKRHRCATVEKENCAPSPLSQ 242
|||
Qy 231 LLVEH 235
|||
Db 243 VTISH 247

RESULT 15

A53137
tyrosine kinase receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A53137
R:Sanchez, M.P.; Tapley, P.; Saint, S.S.; He, B.; Pulido, D.; Barbacid, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994
A:Title: Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-
A:Reference number: A53137; MUID:94173920
A:Accession: A53137
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-910 <RES>
A:Cross-references: GB:L26525; NID:g432480; PIDN:AAA21089.1; PID:g432481
C:Genetics:
A:Gene: Ptk-3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C:Keywords: Atp
F:31-186/Domain: discoidin I amino-terminal homology <DN1>
F:605-909/Domain: protein kinase homology <KIN>
F:613-621/Region: protein kinase ATP-binding motif

Query Match 7.0% Score 87; DB 2; Length 910;
Best Local Similarity 24.5% Pred. No. 15; Mismatches 35; Indels 70; Gaps 9;
Matches 38; Conservative 12
Qy 143 PWITRQNFRCLEQCQPDSTLPP-PW---SPRPLEATA----PTAFQP----- 184
|||
Db 356 PWLLFSEISFISDV-VNDSSDTPTPPAPWPPGPPPTNFSSLELEPRGQOPVAKAGSPTA 414
|||
Qy 185 -----PLLLLLLPVGL LLLAAAWCLHWQRTTRR-----T 214
|||
Db 415 ILIGCLVAIIILLIIIALML----WRLHWRLLSKAERRVLEELAVHLSVPGDTILIN 470
|||
Qy 215 PRGGEQVPP-----VPSQDILL 232
|||
Db 471 NRPGPREPPYQEP RRGTPTHSAPCVNGSALLL 505

Search completed: April 1, 2002, 06:15:21
Job time: 87 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:16:39 ; Search time 68.97 Seconds
(without alignments)
124.927 Million cell updates/sec

Title: US-08-162-407-6

Sequence: 1 MTVLAPAWSPTTLLLLLLL.....RPGQVPPVSPQDILLIVH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1 FL3L_HUMAN	P49771 homo sapien
2	768	61.8	232	1 FL3L_MOUSE	P09772 mus musculus
3	92	7.4	661	1 AT12_VZVD	P09264 varicella-z
4	89.5	7.2	941	1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387	1 SGCA_MESAU	O64255 mesocricetu
6	89	7.2	793	1 S3A1_HUMAN	O15459 homo sapien
7	87.5	7.0	415	1 TNRC_MOUSE	P02884 mus musculus
8	87.5	7.0	479	1 MP1P_DROME	P20483 drosophila
9	87	7.0	910	1 DDRL_MOUSE	Q63474 rattus norv
10	86.5	7.0	1394	1 CNG4_BOVIN	Q03146 mus musculus
11	86	6.9	485	1 SSGP_VOLCA	Q28181 bos taurus
12	85	6.8	282	1 ATF5_HUMAN	O972d1 volvox cart
13	85	6.8	365	1 FCGN_RAT	P13599 rattus norv
14	84	6.8	582	1 MNT_HUMAN	Q99583 homo sapien
15	84	6.8	732	1 YF48_HUMAN	O9hcm4 homo sapien
16	83.5	6.7	671	1 Z282_HUMAN	O9udv7 homo sapien
17	83.5	6.7	758	1 VKGC_HUMAN	P38435 homo sapien
18	83	6.6	488	1 MW11_HUMAN	P24347 homo sapien
19	81.5	6.6	591	1 MNT_MOUSE	O08789 mus musculus
20	81.5	6.6	591	1 MNT_MOUSE	Q93074 homo sapien
21	81.5	6.6	2124	1 Y192_HUMAN	O70191 mus musculus
22	81	6.5	283	1 ATF5_MOUSE	P82350 mus musculus
23	81	6.5	387	1 SGCA_MOUSE	P01854 homo sapien
24	81	6.5	428	1 EPC_HUMAN	O06010 homo sapien
25	81	6.5	1248	1 DIAL_HUMAN	P11110 oryctolagus
26	80.5	6.5	1402	1 IF4G_RABIT	P18549 streptomyce
27	80	6.4	397	1 CEFD_STRCL	O88871 rattus norv
28	80	6.4	940	1 GBR2_RAT	O42632 cochiolobu
29	80	6.4	1174	1 KPCL_COCH	Q01072 schizosacch
30	80	6.4	1794	1 YAV1_SCHPO	P3086 saccharomyc
31	79	6.4	805	1 XGW6_YEAST	P17483 homo sapien
32	78.5	6.3	251	1 HXB4_HUMAN	P38445 rattus norv
33	78.5	6.3	382	1 AVRE_RAT	

34	78.5	6.3	387	1 SGCA_RABIT	Q28686 oryctolagus
35	78.5	6.3	913	1 DDRL_HUMAN	Q08345 homo sapien
36	78.5	6.3	1180	1 ATY1_HUMAN	Q9nq11 homo sapien
37	78	6.3	205	1 CYSR_SYNY3	Q5854 synechocyst
38	78	6.3	566	1 TS13_MOUSE	Q01755 mus musculus
39	77.5	6.2	1885	1 PAS2_CANAL	P43098 c fatty aci
40	77.5	6.2	2004	1 MOZ_HUMAN	Q92794 homo sapien
41	77	6.2	195	1 CORA_HPBVF	P29178 hepatitis b
42	77	6.2	316	1 CONC_HUMAN	P49918 homo sapien
43	77	6.2	367	1 MREC_ECOLI	P16926 escherichia
44	77	6.2	478	1 BM3B_HUMAN	P35107 homo sapien
45	77	6.2	742	1 PKWA_THECU	P49695 thermomonos

ALIGNMENTS

RESULT 1
FL3L_HUMAN
ID FL3L_HUMAN STANDARD; PRT; 235 AA.
AC P49771;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3
DE LIGAND).
GN FLT3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94195428; PubMed-8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kellner G., Namikawa R., Rennick D., Roncarolo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
RT "Ligand for FLT3/Flk2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs."
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94235842; PubMed-8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Spletter R.R., Beckmann M.P., McKenna H.J.,
RT "Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells."
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-96032581; PubMed-7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci."
RL Oncogene 11:1165-1172(1995).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; U04806; AAA17999.1; -
 DR EMBL; U03858; AAA19825.1; -
 DR EMBL; U29874; AAA90949.1; -
 DR EMBL; U29874; AAA90950.1; -
 DR MIN; 600007; -
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 235
 FT DOMAIN 27 184
 FT TRANSMEM 27 205
 FT DOMAIN 206 235
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPPLIC 161 178
 FT VARSPPLIC 179 235
 FT CONFLICT 72 72
 FT SEQUENCE 235 AA; 26416 MW; 73B95BF693B4CECF CRC64;
 SQ
 Query Match 100.0%; Score 1242; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 6.3e-98;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTVLAPAWSPPTLYLLLLLLSGLSGTCDFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 Db 1 MTVLAPAWSPPTLYLLLLLLSGLSGTCDFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 Qy 61 ASNLQDELCGLRLVLAQRWMLKTVAGSKWGLLRYNTEHFYTKAFQPPPSCL 120
 Db 61 ASNLQDELCGLRLVLAQRWMLKTVAGSKWGLLRYNTEHFYTKAFQPPPSCL 120
 Qy 121 RVQNTISRLQETSEQLVALKPWITRQNFSCLELQCPDSSITLPPWSPRPLEATAPT 180
 Db 121 RVQNTISRLQETSEQLVALKPWITRQNFSCLELQCPDSSITLPPWSPRPLEATAPT 180
 Qy 181 AQPPPLLLLLPVGLLLAAWCLHWQTRRRTRPRGQVPPVPSQDILLVEH 235
 Db 181 AQPPPLLLLLPVGLLLAAWCLHWQTRRRTRPRGQVPPVPSQDILLVEH 235
 RESULT 2
 FL3L_MOUSE STANDARD; PRT; 232 AA.
 ID FL3L_MOUSE
 AC P49772;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3 LIGAND).
 DE LIGAND).
 GN FLT3LG OR FLT3L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195428; PubMed=8145851;
 RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
 RA Muench M., Keiner G., Namikawa R., Rennick D., Roncarolo M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
 RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
 RT hematopoietic stem cells and is encoded by variant RNAs.";
 RL Nature 368:643-648(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SJL/J;
 RX MEDLINE=94084791; PubMed=7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spiett R.N., Fletcher F.A., Maraskovsky E., Farran T.,

RA Foxworthe D., Williams D.E., Beckmann M.P.;
 RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RT receptor: a proliferative factor for primitive hematopoietic cells.";
 RL Cell 75:1157-1167(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96032581; PubMed=7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL Oncogene 11:1165-1172(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95124710; PubMed=7824267;
 RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland D.S.;
 RT "Identification of soluble and membrane-bound isoforms of the murine
 RT flt3 ligand generated by alternative splicing of mRNAs.";
 RL Oncogene 10:149-157(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsal S., Luh J., Guimares M.J.,
 RA Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
 CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; U04807; AAA18000.1; -
 DR EMBL; L23636; AAA39436.1; -
 DR EMBL; U29875; AAA90951.1; -
 DR EMBL; U29875; AAA90952.1; -
 DR EMBL; S76459; AAA33069.1; -
 DR EMBL; S76461; AAA33070.1; -
 DR EMBL; U44024; AAA93307.1; -
 DR EMBL; U44024; AAA93306.1; -
 DR MGD; MGI:95560; Flt3l.
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 232
 FT DOMAIN 27 189
 FT TRANSMEM 190 210
 FT TRANSMEM 211 232
 FT DOMAIN 211 232
 FT CARBOHYD 127 127
 FT CARBOHYD 152 152
 FT VARSPPLIC 164 232
 FT VARSPPLIC 164 169
 FT VARSPPLIC 170 232
 FT CONFLICT 141 141
 FT CONFLICT 198 198
 FT SEQUENCE 232 AA; 26141 MW; 3A3680D3CB69FBA6 CRC64;
 SQ
 Query Match 61.8%; Score 768; DB 1; Length 232;
 Best Local Similarity 70.0%; Pred. No. 5.9e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 10; Gaps 4;

```
QY 1 MTVLAPAWSP-TTYLLLLSSLSGTCQDSFQSPISDFAVKIRELSYLLQDYPVT 59
Db 1 MTVLAPAWSPSSLLLLLLSCLRCPTDCYFSHSPISSNFKVKFRELTDHLLKDPVT 60
QY 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIHFTVKCAFPSPSC 119
Db 61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMGLLERNVTEIHFTVCTFQPLPEC 120
QY 120 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCRLELOCQDSSSLPLPPWSPRPLEAT 177
Db 121 LRFVQTNISHLKTDCTQLLALAPCIGKACQNFSCRLEVCQDSSSTLLPPRSPALEAT 180
QY 178 APTAPOP---LLLLLLPVGLLLAAWCLHWQTRRRTPRGEQVPPVPS 227
Db 181 ELPEPRPQRLLLLLLLPVLVLLAAWGLRQARRR---GELHPGVLP 229

RESULT 3
AT12_VZVD
ID AT12_VZVD STANDARD; PRT; 661 AA.
AC P09264;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 01-NOV-1990 (Rel. 16, Last annotation update)
DE ALPHA TRANS-INDUCING FACTOR 74 KDA PROTEIN.
GN 12.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8630657; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
CC ACTIVATION OF ALPHA GENES
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04370; CAA27895.1; -
DR PIR; C27342; TNBE12.
KW Transcription regulation; Trans-acting factor.
SQ SEQUENCE 661 AA; 74272 MW; C5CA77A16D365379 CRC64;

Query Match 7.48; Score 92; DB 1; Length 661;
Best Local Similarity 26.68; Pred. No. 2.1;
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

QY 19 LLSGLSGTQDCS-----FOHSPISDFAVKI--RELSYLLQDYPVTVASNLQDELCG- 71
Db 79 LTPVLQSTHERSHVLLGLHNNVPESLVSCMSNDVDFGMQRYMETIQRCLDLKLSGD 138
QY 72 GLWRLVLAQRWMLKTVAGSKMGLLERNV-----TEIHFTVKCAFP-----PSCSLRFV 123
Db 139 GLW-WYVNTYVQWLKTTGAQVPTVSEKVNKSKSTVLLFSSVAVANKPIRHPFKSVI 197
QY 124 QTNISRLQETSEQLVALKPWITRQNFSCRLELOCQDSSSLPLPPWSP-RELEATAPAT 182
Db 198 NSDVRGICQELREALGAVQYK-----YFWR-----PDDTNPSPDTRIRVQIEAATAT 247
QY 183 OPPELLLLLPVGLLLAAWCLHWQTRRRTPRPGQVPPVPSQDILL 231
Db 248 GYGWMLWFLDWD-----ARVCRHLKQFRRIRPRASV---IPDDL 287
```

```
RESULT 4
GBR2_HUMAN STANDARD; PRT; 941 AA.
ID GBR2_HUMAN
AC 075899; 075974; 075975; Q9UN9S; Q9UNR1; Q9PLR2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR
DE 51) (GPR 51) (HC20).
GN GABR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emsen P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Fetal brain;
RX MEDLINE=99189236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1.";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
```


RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation of the same gene, delta-sarcoglycan, in hamster: an animal model of disrupted dystrophin-associated glycoprotein complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FIB: TISSUE-Skeletal muscle;
 RA MEDLINE=95278335; PubMed=7758576;
 RX Roberts S.L., Campbell K.P.;
 RT "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.";
 RL FEBS Lett. 364:245-249(1995).
 CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMMA (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND HEART MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL: D83651; BAA12025.1;
 CC EMBL: U21677; AAA81645.1;
 KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 387 ALPHA-SARCOGLYCAN.
 FT DOMAIN 24 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 291 311 POTENTIAL.
 FT DOMAIN 312 387 POTENTIAL.
 FT DOMAIN 209 335 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 174 174 CYS-RICH.
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.2%; Score 89; DB 1; Length 387;
 Best Local Similarity 23.4%; Pred. No. 2;
 Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;
 QY 11 TTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPYVTVASNLQDEELC 70
 Db 115 TTRQLLLLI-----EDPEGRLPYQAEFLVRSHDVEYL----PSTPANREL--TAL 161
 QY 71 GGLWRL-----VLAQRWMLKTVAGSKMGLLRVNTIHFVT-----K 110
 Db 162 GGLWELGELQLNLTSLDRGRVPLTEGRKEGYIKVGSATFSTCLKWVSPDSVAR 221
 QY 111 CATQPPP--SC-----LRFVNINISRLLOETSEQLVALKPWITRQNSRCLQCOPD 161
 Db 222 CAQCQPPLLSCYSLAPHFRVDMCNVSLDKSVPELD-----EVPTPGD 266
 QY 162 SSTLPWPSPRPLEAT-----APTAPQPLLLLLLVGLLLLLAANC----- 204
 Db 267 GILEHDFCFPCPTAQRDLADALVTLVPLLVALLL---TLLAVIMCRRREGQLKRD 323
 QY 205 -----LHWQTRRRTRPR-----GEQVPP--VPSPQ--DLL 231
 Db 324 MATSDIQMVHCHTGHNGTEELRQMAARVPRPLSTLPMFNVRTGERLPPRVDSQAQVPLI 383
 QY 232 LVHE 235
 Db 384 LDQH 387
 RESULT 6

S3A1_HUMAN
 ID S3A1_HUMAN STANDARD; PRT; 793 AA.
 AC Q15459;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SPLICING FACTOR 3 SUBUNIT 1 (SPliceosome ASSOCIATED PROTEIN 114) (SAP 114) (SF3A120).
 GN SF3A1 OR SAP114.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079958; PubMed=7489498;
 RA Kraemer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;
 RT "Mammalian splicing factor SF3a120 represents a new member of the SURP family of proteins and is homologous to the essential splicing factor PRP21p of Saccharomyces cerevisiae.";
 RL RNA 1:260-272(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bentley D., Blandford M.;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION OF THE SPLICESOME.
 RX PubMed=10882114;
 RA Das R., Zhou Z., Reed R.;
 RT "Functional association of U2 snRNP with the ATP-independent Mol. Cell 5:779-787(2000).
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF THREE SUBUNITS; SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP). INTERACTS WITH SF3A3.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL: X85237; CAA59494.1;
 CC EMBL: AC004997; AAC23435.1;
 CC MIN; 605595;
 DR InterPro; IPR000061; Surp.
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF01805; Surp; 2.
 DR Pfam; PF00240; ubiquitin; 1.
 DR SMART; SM00213; UBO; 1.
 DR PROSITE; PS0053; UBQUITIN_2; 1.
 DR SPLICesome; mRNA processing; Nuclear protein; Repeat.
 KW REPEAT 52 94 SURP MOTIF 1.
 FT REPEAT 166 208 SURP MOTIF 2.
 FT DOMAIN 707 793 UBQUITIN-LIKE.
 FT DOMAIN 10 16 POLY-PRO.
 FT DOMAIN 118 122 POLY-GLN.
 FT DOMAIN 260 267 POLY-GLU.
 FT DOMAIN 369 372 POLY-PRO.

FT DOMAIN 557 560 POLY-PRO.
FT DOMAIN 672 675 POLY-PRO.
SQ SEQUENCE 793 AA; 8886 MW; 7259F1EC4577305C CRC64;

Query Match 7.2%; Score 89; DB 1; Length 793;
Best Local Similarity 22.3%; Pred. No. 4.6;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPANSPYTYLLLLLLSGLSGTQDCSQHSPISSDFAVKRIELSDYLLQDPVTVASN 63
DB 401 LPPAPADYLV-----SPITGE---KI-----PASK 424
QY 64 LQDEELCGGLWRLVLAQRWME-RLKTV-----AGSKMOGLLERNVTEIHF 107
DB 425 MOEHMRIG-----LLDPRLWLEQDRSIREKQSDVEYAPGLDIESLKQLAER-RDIFG 478
QY 108 VTKCA-----FQPPPSCLRF-----VOTNISRLQETSEQLVALKPW 145
DB 479 VEETAIGKIGBEEIQPEKVTWDHSGSMARTQQAQANIT--LQEQIEAIHKAGLV 536
QY 146 ----TRQNF--SRCELOQCP-----DSTLP-----PPSPRPLEAT----APT 180
DB 537 PEDTKEKIGSKPNRIPPOPPPSATIPSPRPTTSVPRPPTMPPPVRTVWSAVPV 596
QY 181 APQPPPLLLLLPVGLLLAAAWCLHWQTR-----RRTPRPGQVPP---VPSP 227
DB 597 MRPPMASVVRLLPGSVIAPMPPIIHAPINVPMPSPAPPINAPRPPMIVPTAFVAP 656

RESULT 7
TNRC_MOUSE
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8596432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----

DR EMBL: U29173; AA68964.1; --
DR EMBL: L38423; AA00846.1; --
DR EMBL: U30798; AA81334.1; --
DR HSSP: P25942; ICDF.
DR MGD: MGI:104875; Ltbr.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;
Best Local Similarity 24.4%; Pred. No. 2.9;
Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFPQPPSCL-----RFV-----QTNISRLQETSEQLVALKPWITRQNF 151
DB 123 ECRQCPGMSCVLDNECVHCEERLVLCQGTAEVDEIMDVCNVCYPCPKPGHQNTSS 182
QY 152 RCLELOCQDPSSTLPPWSPRPLEATP-----TAPQPLLLLLLPVGLL--- 198
DB 183 P--RARCQPHTRC-----EQGLVEAAAGTSYSDTICKNPPEGAMLLAILLSLVFL 235
QY 199 ----LAAAWCLHWQTR-----RRTPRPGQVPPVPSQ 228
DB 236 FTTVLACAMRHPSLCKRLKLTLLKRHPE-GEESPPCPAPR 274

RESULT 8
MP1P_DRONE
ID MP1P_DRONE STANDARD; PRT; 479 AA.
AC P20483; Q9VAL9;
DT 01-FEB-1991 (Rel. 17, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE M-PHASE INDUCER PHOSPHATASE (EC 3.1.3.48) (STRING PROTEIN) (CDC25-LIKE
DE PROTEIN).
GN STG OR CDC25 OR CGL395.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89195217; PubMed=2702688;
RA Edgar B.A., O'Farrell P.H.;

"Genetic control of cell division patterns in the Drosophila embryo."
Cell 57:177-187(1989).

[2]
SEQUENCE FROM N.A.
MEDLINE=91006056; PubMed=2120044;
Jinenez J., Alpheley L., Nurse P., Glover D.M.;
"Complementation of fission yeast cdc2ts mutants
identifies two cell cycle genes from Drosophila: a cdc2 homologue and
string.";
EMBO J. 9:3565-3571(1990).

[3]
SEQUENCE FROM N.A.
SPRAIN-BERKELEY;
MEDLINE=20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Duncan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarri K., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Pan S.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).

-1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.

-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O =
PROTEIN TYROSINE + ORTHOPHOSPHATE.

-1- SIMILARITY: STRONG. TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; M24903; AAA28916.1;
EMBL; X57495; CAA40732.1;
EMBL; AE003768; AAF56885.1;
PIR; A32290; A32290.

DR PIR: S12008; S12008.
DR HSP: P30304; IC25.
DR FlyBase; FBgn0003325; stg.
DR InterPro; IPR000751; MPI_Phosphatase.
DR Pfam; PF00581; Rhodanese_1.
DR PRINTS; PR00716; MEIPHPHATASE.
DR SMART; SM00450; RHOD; 1.
KW Cell division; Mitosis; Hydrolase.
FT ACT-SITE 379
FT CONFLICT 228 228 A -> T (IN REF. 1).
SQ SEQUENCE 479 AA; 54094 MW; 68483F3A285962CC CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 479;
Best Local Similarity 22.9%; Pred. No. 3.4;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MTVLAPAGPTTYLL--LLLSLSSGSGQDCSFQHSPISSDPFAVKIRELSYLLQDYP 57
Db 72 MGLSPGSGFQFQIVQPKILPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
QY 58 VTVASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMOGLERVTETHFVTRCAFP 117
Db 118 CSMESSMDDE-----YMLFEMESQSQ-----QTALGF-----P 146
QY 118 SCLRFQVQTNISRLQTSBOLVALKP---WITRNFNSRCLLEL-QCOPDSSTLPPWSPRP 173
Db 147 SGLN-----SLISGQIKQPAKSPAGLSMRPSVRCLSMTESNTNSTTTPPKTPE- 199
QY 174 LEATAPTA---PPPLLLLLLLPVGLLLAAACLWQRTTRTPRPGQVPPVPSQDL 230
Db 200 ---TARDCKFRPEPP-----ASANCSPQSRKRCRAAVERKNCAPSPLSQ 242
QY 231 LLVEH 235
Db 243 VVISH 247

RESULT 9

DDRL_RAT
ID DDRL_RAT STANDARD; PRT; 910 AA.
AC Q63474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EPIHETIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
DE (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE
DE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE
DE PTK-3).
GN DDRL OR EDDRL OR PTK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=94173920; PubMed=8127887;
RA Sanchez M.P., Tapley P., Saini S., He B., Pulido D., Barbacid M.;
RT "Multiple tyrosine protein kinases in rat hippocampal neurons:
RT isolation of Ptk-3, a receptor expressed in proliferative zones of
RT the developing brain."
RL Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.

DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 1.
 KW Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
 KW Phosphorylation; Transmembrane; Receptor; ATP-binding;
 KW Alternative splicing.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 911 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
 FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 415 441 POTENTIAL.
 FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 186 F5/8 TYPE C (PHOSPHOLIPID-BINDING, POTENTIAL).
 FT DOMAIN 379 413 GLY/PRO-RICH.
 FT DOMAIN 474 599 GLY/PRO-RICH.
 FT DOMAIN 608 903 PROTEIN KINASE.
 FT NP_BIND 614 622 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 764 764 BY SIMILARITY.
 FT DISULFID 32 186 BY SIMILARITY.
 FT MOD_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 503 539 MISSING (IN ISOFORM CAK II).
 SQ SEQUENCE 911 AA; 101160 MW; DB7FE03DD79510 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 911;
 Best Local Similarity 24.5%; Pred. No. 8;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

Qy 143 PWITQNSRCLQCPDSSLLP-PW---SPRPLEATA---PTAPQP-----184
 Db 357 PMLFSEISFISDV-VNDSDTFPPAPWPPGPPPTNFSLEPRGQPVAKAEGSPTA 415
 Qy 185 -----PLLILLPVGLLLAAWCLHWQR-----TRRR-----T 214
 Db 416 ILIGLVAILLLLIALLML-----WRLHWRLLSKAERVLEELTVHLSVPGDITLIN 471
 Qy 215 PRPGQVPP-----VPSQDILL 232
 Db 472 NRPGPREPPYQEPRTGTPPHSAFCVNGSALLL 506

RESULT 11
 CNG4_BOVIN STANDARD; PRT; 1394 AA.
 AC Q28181; Q28082; 003861.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 240 KDA PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].
 DE CNGB1 OR CNGC4.
 GN Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=96009859; PubMed=7546742;
 RA Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
 RA Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
 RA Kaupp U.B., Molday R.S.;
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";

Neuron 15:627-636(1995).
 [2]
 RN SEQUENCE OF 454-1394 FROM N.A.
 RP TISSUE-Testis;
 RC MEDLINE=96198098; PubMed=8626431;
 RX Biel M., Zong X., Ludwig A., Sautter A., Hofmann F.;
 RA "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
 RN J. Biol. Chem. 271:6349-6355(1996).
 [3]
 RN SEQUENCE OF 1-590 FROM N.A.
 RP TISSUE-Retina;
 RC Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
 RA Submitted (XX-1991) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBUNIT: FORMS FUNCTIONAL HETEROLOGIC CHANNELS WITH CNG3.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: CNG4C (SHOWN HERE), CNG4D, AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.
 CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; X89626; CAA61769.1; .
 DR EMBL; X94707; CAA64367.1; .
 DR EMBL; M61185; CAA30536.1; .
 DR InterPro; IPR002025; CNG_membrane.
 DR InterPro; IPR000595; CNGP_binding.
 DR Pfam; PF00914; CNG_membrane; 1.
 DR Pfam; PF00027; CNGP_binding; 1.
 DR SMART; SM00100; CNGP; 1.
 DR PROSITE; PS00889; CNGP_BINDING_1; 1.
 DR PROSITE; PS00889; CNGP_BINDING_2; 1.
 DR PROSITE; PS50042; CNGP_BINDING_3; 1.
 KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
 KW Multigene family; Alternative splicing.
 FT CHAIN 1 590 GLUTAMIC ACID-RICH PROTEIN.
 FT CHAIN 454 1394 CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4.
 FT DOMAIN 1 767 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 768 786 H1 (POTENTIAL).
 FT DOMAIN 787 800 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 801 819 H2 (POTENTIAL).
 FT DOMAIN 821 844 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 845 864 H3 (POTENTIAL).
 FT DOMAIN 865 901 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 902 924 H4 (POTENTIAL).
 FT DOMAIN 925 968 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 969 988 H5 (POTENTIAL).
 FT DOMAIN 989 1072 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1073 1093 H6 (POTENTIAL).
 FT DOMAIN 1094 1394 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 1081 1219 CAMP (BY SIMILARITY).
 FT BINDING 1141 1141 CAMP (POTENTIAL).
 FT BINDING 1153 1153 CAMP (POTENTIAL).
 FT CARBOHYD 1067 1067 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 515 532 MISSING (IN ISOFORM CNG4E).
 FT VARSPPLIC 522 530 MISSING (IN ISOFORM CNG4D).
 FT CONFLICT 341 341 K -> E' (IN REF. 3).
 FT CONFLICT 454 465 REEEDDEEEED -> MRAGQGR (IN REF. 2).
 FT CONFLICT 482 482 R -> Q (IN REF. 2 AND 3).
 FT CONFLICT 499 499 A -> T (IN REF. 3).
 FT CONFLICT 572 590 VPATEEHPQLQVEDADDS -> GSQMSPFALQCEALK R (IN REF. 3).
 FT CONFLICT 1283 1283 S -> A (IN REF. 2).
 FT CONFLICT 1289 1289 R -> A (IN REF. 2).

LIKE HETERODIMER.

- 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- 1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
- 1- SIMILARITY: STRONG, TO MHC CLASS I ANTIGENS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X14323;	CAG32503.1;	--
EMBL; M35495;	AAA41611.1;	--
PIR; S02117;	S02117.	
PIR; A37374;	A37374.	
PDB; 1FR7*	14-FEB-95.	
PDB; 3FRU;	10-JUN-98.	
InterPro; IPR003006;	Ig_MHC.	
InterPro; IPR003597;	Ig_cI.	
InterPro; IPR001220;	Lectin_legB.	
InterPro; IPR001039;	MHC_I.	
Pfam; PF00047;	Ig; 1.	
Pfam; PF00129;	MHC_I; 1.	
ProDom; PD000050;	MHC_I; 1.	
SMART; SM00407;	IGc1; 1.	
PROSITE; PS00290;	IG_MHC; 1.	

Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
immunoglobulin domain; 3d-structure.

	FT SIGNAL	1	22	
FT CHAIN	23	366		IGG RECEPTOR FCERN LARGE SUBUNIT P51.
FT DOMAIN	23	111		EXTRACELLULAR ALPHA-1.
FT DOMAIN	112	201		EXTRACELLULAR ALPHA-2.
FT DOMAIN	202	231		EXTRACELLULAR ALPHA-3.
FT DOMAIN	292	298		CONNECTING PEPTIDE.
FT TRANSMEM	299	322		POTENTIAL.
FT DOMAIN	323	366		CYTOPLASMIC (POTENTIAL).
FT DISULFID	120	183		BY SIMILARITY.
FT DISULFID	222	276		BY SIMILARITY.
FT CARBOHYD	109	109		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	126	126		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	150	150		N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	247	247		N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE	366 AA;	40168 MW;	8ABBF2873A698BB5 CRC64;	

	Query Match	6.8%; Score 85;	DB 1;	Length 366;
	Best Local Similarity	22.2%;	Pred. No. 4.1;	
	Matches 51;	Conservative 21;	Mismatches 66;	Indels 92; Gaps 11;

QY	46	RELSDYLLODPVTVASNLDEELCGGLRWLYLAQRWE----	RLKTVAGSKMOGLLEVV 101
Db	173	KRESEFLTSCTP-----ERLLGHLEGRQNLEWKPEPSMRLKARPNGSSSVL---	220
QY	102	NTEIHFTVKCA---EQPPSPCLRFVTNLSRLLETSEQVLAKPWITRNQSFRC-----	153
Db	221	-----TCAAFSVPPELPKFFRLNGLA-----SGSGNCSTGN 253	
QY	154	-----LEL-----OCQPDSSLTLPWPSPRPLEATAPAPOLLLLLLLVPG 195	
Db	254	GDSGFSAWSLLEVKGDEHHYOQVEHGLEAQPLT---VDLDSPARSVPVVGII--G 307	
QY	196	LLLLA---AAWCLHWQRTERRTTPR-----PGEQVPPVPSQ 228	
Db	308	LLLVAIAAGVLLWNRMRSGLPAFWLSLGDDSGDLLPGGNLLPPEAEFQ 357	


```

RESULT 15
MNT_HUMAN
IID MNT_HUMAN STANDARD; PRS; 582 AA.
AC Q99583;
DT 15-DEC-1998 (Rel. 37, Created)
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 64.79 seconds
(without alignments)
81.622 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPTTYLLLLLLL.....RPGQVPPVSPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2.6/prodata/2/1aa/5A-COMB.pep.*
2: /cgn2.6/prodata/2/1aa/5B-COMB.pep.*
3: /cgn2.6/prodata/2/1aa/6A-COMB.pep.*
4: /cgn2.6/prodata/2/1aa/6B-COMB.pep.*
5: /cgn2.6/prodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2.6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1 US-08-243-545-6	Sequence 6, Appl
2	1242	100.0	235	2 US-08-993-962-6	Sequence 6, Appl
3	1242	100.0	235	4 US-09-160-841-6	Sequence 6, Appl
4	1242	100.0	235	4 US-09-109-100-1	Sequence 1, Appl
5	1242	100.0	235	5 PCT-US94-05365-6	Sequence 6, Appl
6	1124	90.5	212	4 US-09-109-100-10	Sequence 10, Appl
7	1114	89.7	209	4 US-09-109-100-18	Sequence 18, Appl
8	1110	89.4	209	4 US-09-109-100-9	Sequence 9, Appl
9	1110	89.4	209	4 US-09-109-100-12	Sequence 12, Appl
10	1110	89.4	209	4 US-09-109-100-14	Sequence 14, Appl
11	1110	89.4	209	4 US-09-109-100-17	Sequence 17, Appl
12	1108	89.2	209	4 US-09-109-100-11	Sequence 11, Appl
13	1108	89.2	209	4 US-09-109-100-15	Sequence 15, Appl
14	1107	89.1	209	4 US-09-109-100-13	Sequence 13, Appl
15	1106	89.0	209	4 US-09-109-100-8	Sequence 8, Appl
16	1100	88.6	209	4 US-09-109-100-16	Sequence 16, Appl
17	768.5	61.9	231	1 US-08-243-545-2	Sequence 2, Appl
18	768.5	61.9	231	2 US-08-993-962-2	Sequence 2, Appl
19	768.5	61.9	231	4 US-09-160-841-2	Sequence 2, Appl
20	768.5	61.9	231	5 PCT-US94-05365-2	Sequence 2, Appl
21	765.5	61.6	231	1 US-08-220-379B-7	Sequence 7, Appl
22	765.5	61.6	231	5 PCT-US95-03866-6	Sequence 6, Appl
23	506.5	40.8	137	4 US-09-109-100-19	Sequence 19, Appl
24	154	12.4	42	5 PCT-US94-05150-17	Sequence 17, Appl
25	91.5	7.4	675	1 US-08-317-522A-9	Sequence 9, Appl
26	91.5	7.4	675	1 US-08-439-818A-9	Sequence 9, Appl
27	91.5	7.4	675	2 US-08-751-965-9	Sequence 9, Appl

28 91.5 7.4 675 2 US-08-738-975-9 Sequence 9, Appl
29 91.5 7.4 675 2 US-08-728-626-9 Sequence 9, Appl
30 91.5 7.4 675 2 US-08-808-599A-9 Sequence 9, Appl
31 87.5 7.0 415 4 US-09-006-353A-6 Sequence 6, Appl
32 85 6.8 366 1 US-08-004-493-8 Sequence 8, Appl
33 84.5 6.8 913 1 US-08-445-580-4 Sequence 4, Appl
34 84.5 6.8 913 3 US-08-170-558-4 Sequence 4, Appl
35 84.5 6.8 913 3 US-08-447-314-4 Sequence 4, Appl
36 84.5 6.8 913 3 US-08-445-461-4 Sequence 4, Appl
37 84 6.8 107 4 US-09-220-528-52 Sequence 52, Appl
38 84 6.8 220 4 US-09-220-528-26 Sequence 26, Appl
39 83.5 6.7 429 1 US-07-964-582-2 Sequence 2, Appl
40 83.5 6.7 429 5 PCT-US93-02024-2 Sequence 2, Appl
41 83.5 6.7 671 3 US-09-121-321-16 Sequence 16, Appl
42 83.5 6.7 671 4 US-08-933-803A-16 Sequence 16, Appl
43 83 6.7 28 5 PCT-US94-05150-12 Sequence 12, Appl
44 83 6.7 758 1 US-07-756-250-16 Sequence 16, Appl
45 82.5 6.6 249 2 US-08-632-514C-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-243-545-6

Query Match      100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
Db 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLRWLRVLAQRWMERLKTAVAGSKMOGLLERVNTFHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLRWLRVLAQRWMERLKTAVAGSKMOGLLERVNTFHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235

RESULT 2
US-08-993-962-6
; Sequence 6, Application US/08993962
; Patent No. 5843423
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,962
; FILING DATE: December 18, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644

;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-962-6

Query Match      100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
Db 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLRWLRVLAQRWMERLKTAVAGSKMOGLLERVNTFHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLRWLRVLAQRWMERLKTAVAGSKMOGLLERVNTFHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235

RESULT 3
US-09-160-841-6
; Sequence 6, Application US/09160841
; Patent No. 6190655
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0430
```

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMQLLVRNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMQLLVRNTEIHFVTKCAFQPPPSCL 120
QY 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
DB 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
QY 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235
DB 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

RESULT 4

US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMQLLVRNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMQLLVRNTEIHFVTKCAFQPPPSCL 120
QY 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
DB 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
QY 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235
DB 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

RESULT 5

PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY	27	TQDCSFQHSPISSDFAYKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAQRWML	86
Db	1	TQDCSFQHSPISSDFAYKIRELSYLLQDYPVTVASNLQDEELCGGLRWLVLAQRWML	60
QY	87	KTVAGSKMQLLVRVNTIEHFVTKCAFQPPSPCLRFVQTNISRLQTSQVLVAKPWIT	146
Db	61	KTVAGSKMQLLVRVNTIEHFVTKCAFQPPSPCLRFVQTNISRLQTSQVLVAKPWIT	120
QY	147	RQNFSCRLELQCPDSTLPPPPNSPRPLEATAPTAPOPPLLLLLLPVGLLLAAACWCH	208

Db 121 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 180
QY 207 WORTRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WORTRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 180
QY 207 WORTRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WORTRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 180
QY 207 WORTRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WORTRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.1e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRPLEATAPOPPPLLLLLLPGVLLLLAAACWLH 180
QY 207 WORTRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WORTRRTPRGEQVPPVSPQDLLLLVEH 209

Search completed: April 1, 2002, 06:16:38
Job time: 164 sec

